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(54) Title: REAGENTS AND METHODS FOR INHIBITING FURIN PROTEASE ACTIVITY

(57) Abstract

This invention relates to methods and reagents for inhibiting furin endoprotease activity and specifically for inhibiting furin endoprotease-mediated maturation of bioactive proteins *in vivo* and *in vitro*. The invention specifically provides peptides, peptide analogues, peptide derivatives and peptido-, organo- and chemical mimetics of said peptide inhibitors of furin endoprotease activity. Methods for using furin endoprotease inhibition to attenuate or prevent viral protein maturation, and thereby alleviate viral infections, are provided. Also provided are methods for using furin endoprotease inhibition to attenuate or prevent proteolytic processing of bacterial toxins, thereby alleviating bacterial infections methods are also provided to inhibit proteolytic processing biologically active proteins and peptides. The invention also provides pharmaceutically acceptable compositions of therapeutically effective amounts of furin endoprotease inhibitors.

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REAGENTS AND METHODS FOR INHIBITING FURIN PROTEASE ACTIVITY

This application claims priority to U.S. Serial No. 60/081,034, filed April 8, 1998.

This invention was made with government support under DK44629 and DK37274 from the National Institutes of Health. The government has certain rights in the invention.

BACKGROUND OF THE INVENTION

1. Field of the Invention

This invention relates to endoproteases, particularly a novel endoprotease termed furin endoprotease. The invention specifically relates to inhibitors of furin endoprotease activity. In particular, the invention relates to peptides and peptide mimetics derived from a novel variant of $_1$-antitrypsin that specifically inhibit furin endoprotease activity. The invention also provides methods for using such inhibitors to attenuate or prevent biological proteolytic maturation of bioactive proteins and peptides *in vivo* and *in vitro*, in particular with respect to viral proteins and bacterial toxins. Therapeutic methods and pharmaceutical compositions of such inhibitors are also provided directed towards the alleviation and treatment of disease having microbiological etiology.

2. Background of the Related Art

Most biologically active peptides and proteins are synthesized initially as larger, inactive precursor proteins that are endoproteolytically cleaved during transit through the secretory pathway in the Golgi apparatus in cells expressing such proteins (*see* Barr, 1991, *Cell* 66: 1-3 for review). This system comprises an important common mechanism required for synthesis of biologically active proteins and peptides in yeast (Fuller *et al.*, 1988, *Ann. Rev. Physiol.* 50: 345-362), invertebrates (Scheller *et al.*, 1983, *Cell* 32: 7-22) and mammalian cells (Sossin *et al.*, 1989, *Neuron* 2: 1407-1417). Examples of peptides and proteins produced *in vivo* by exocytotic transport through the

Golgi are precursors of peptide hormones, neuropeptides, growth factors, coagulation factors, serum albumin, cell surface receptors, and adhesion molecules.

Morrison *et al.*, 1985, *J. Virol.* 53: 851-857 disclose that F protein of Newcastle disease virus is processed through the exocytotic transport pathway in infected cells.

Perez & Hunter, 1987, *J. Virol.* 61: 1069-1614 disclose that the Rous sarcoma virus (RSV) glycoprotein is processed through the exocytotic transport pathway in infected cells.

Yamada *et al.*, 1988, *Virology* 165: 268-273 disclose that F protein of mumps virus is processed through the exocytotic transport pathway in infected cells.

Randolph *et al.*, 1990, *Virology* 174: 450-458 disclose that the prM protein of flaviviruses is processed through the exocytotic transport pathway in infected cells.

A common structural feature of molecules processed through the exocytotic transport pathway is the presence of basic residues or pairs of basic residues at the proteolytic processing site in the molecule. Examples include serum factors (Factors IX; Bentley *et al.*, 1986, *Cell* 45:343-348; proalbumin; Knowlese *et al.*, 1980, *Science* 209: 497-499; pro-von Willibrand factor; Bonthron *et al.*, 1986, *Nature* 324: 270-273), viral polyproteins (human immunodeficiency virus (HIV) gp160; McCune *et al.*, 1988, *Cell* 53: 55-67; RSV envelope protein; Perez & Hunter, 1987, *J. Virol.* 61: 1609-1614; yellow fever virus protein; Rice *et al.*, 1985, *Science* 229: 726-733; measles virus protein; Richardson *et al.*, 1986, *Virology* 155: 508-523; mumps virus protein; Waxham *et al.*, 1987, *Virology* 159: 381-389; human cytomegalovirus protein; Spaete *et al.*, 1990, *J. Virol.* 64: 2922-2931; varicella zooster virus protein; Keller *et al.*, 1986, *Virology* 152: 181-191), growth factors (preprotransforming growth factor β; Gentry *et al.*, 1988, *Molec. Cell. Biol.* 8:4162-4168; epidermal growth factor; Gray *et al.*, 1983, *Nature* 303: 722-725; pro-β-nerve growth factor (NGF); Edwards *et al.*, 1988, *Molec. Cell Biol.* 8: 2456-2464), receptors (insulin receptor; Yoshimasa *et al.*, 1988, *Science* 240: 784-787); and bacterial toxins (*see* Stephen & Pietrowski, 1986, Bacterial Toxins, 2d ed. (Amer. Soc. Microbiol. Washington, D.C.) *for review*; anthrax toxin; Singh *et al.*, 1989, *J. Biol. Chem.* 264: 11099-11102). The proteolytic processing site has been identified in some of these molecules.

Berger & Shooter, 1977, *Proc. Natl. Acad. Sci. USA* 74: 3647-3651 disclose the sequence –RSKR- at the proteolytic processing site of pro-β-NGF.

Bentley *et al.*, 1986, *ibid.*, disclose the sequence –RPKR- at the proteolytic processing site of the blood coagulation factor protein Factor IX.

McCune *et al.*, 1988, *ibid.*, disclose the sequence –REKR- at the proteolytic processing site of HIV gp160.

Clepak *et al.*, 1988, *Biochem. Biophys. Res. Comm.* 157: 747-754 disclose the sequence –RVRR- at the proteolytic processing site of diphtheria toxin.

Vey *et al.*, 1992, *Virology* 188: 408-413 disclose the sequence –RX(R/K)R- at the proteolytic processing site of influenza hemagglutinin.

Ogata *et al.*, 1990, *J. Biol. Chem.* 265: 20678-20685 disclose the sequence –RSKR- at the proteolytic processing site of *Pseudomonas* exotoxin A.

Klimpel *et al.*, 1992, *Proc. Natl. Acad. Sci. USA* 89: 10277-10281 disclose the sequence –RX(R/K)R- at the proteolytic processing site of anthrax protective antigen.

A cellular endoprotease termed furin has been identified that specifically recognizes the recognition sequence of proteins processed through the exocytotic secretory pathway (Wise *et al.*, 1990, *Proc. Natl. Acad. Sci. USA* 87: 9378-9382; Bresnanhan *et al.*, 1990, *J. Cell Biol.* 111: 2851-2859). This endoprotease is a subtilisin-related, calcium-dependent serine protease (Bresnahan *et al.*, *ibid.*). A complementary DNA copy of the mRNA encoding this endoprotease has been isolated (Wise *et al.*, *ibid.*) and sequenced (van den Ouweland *et al.*, 1992, *Nucleic Acids Res.* 18: 664) and expressed in heterologous cells (Bresnahan et al., ibid). These studies have localized furin by fluoresence immunohistochemistry to the Golgi apparatus of cells expressing this endoprotease (Bresnahan *et al.*, *ibid.*). Furin has been shown to be capable of proteolytically cleaving a number of exocytotically processed proteins.

Bresnahan *et al.*, *ibid.*, disclosure furin-mediated cleavage of pro-β-NGF.

Wise *et al.*, *ibid.*, disclose furin-mediated cleavage of pro-von Willibrand factor and complement factor C3.

Hosaka *et al.*, 1991, *J. Biol, Chem.* 266: 12127-12130 disclose furin-mediated cleavage of renin.

Steineke-Grober *et al.*, 1992, *EMBO J.* 11: 2407-2414 disclose furin-mediated cleavage of influenza hemagglutinin.

Klimpel *et al.*, 1992, *Proc. Natl. Acad. Sci. USA* 89: 10277-10281 disclose furin-mediated cleavage of anthrax protective antigen.

Molloy *et al.*, 1992, *J. Biol. Chem.* 267: 16396-16402 disclose furin-mediated cleavage of anthrax protective antigen.

Klimpel *et al.*, 1992, *Annual Meeting, Amer. Soc. Microbiol.* Abst. B-32 disclose furin-mediated cleavage of diphtheria toxin.

One of the present inventors has discovered a mutated variant of α_1-antitrypsin that effectively inhibits furin endoprotease, termed α_1-antitrypsin Portland (also termed PDX; SEQ ID No.: 1), as disclosed in U.S. Patent 5,604,210, issued February 18, 1997 and International Application, Publication No. WO 94/16073, published July 21, 1994, the complete disclosure of each of which are explicitly incorporated herein in its entirety. This variant has been genetically-engineered to contain Ala_{355} -> Arg_{355} and Met_{358} -> Arg_{358} mutations, whereby the native sequence of α_1-antitrypsin is changed from -Ala_{355}-Ile-Pro-Met_{358}- (SEQ ID No. 2) to -Arg_{355}-Ile-Pro-Arg_{358}- (SEQ ID No. 3) in the Portland variant.

Furin can also be inhibited by specific peptidyl chloroalkylketones (Garten *et al.*, 1989, *Virology* 172: 25-31; Molloy *et al.*, *ibid.*; Hallenberger *et al.*, 1992, *Nature* 360: 358-361), but these substances are toxic in vivo.

In view of the importance of furin endoprotease in activation of bacterial toxins, viral structural proteins and bioactive molecules, there is a need for the development of safe and specific furin inhibitors for prophylaxis, therapy and biological regulation.

SUMMARY OF THE INVENTION

This invention provides safe, specific and effective inhibitors of furin endoprotease that are peptides and peptide mimetics of novel variants of the naturally-occurring protease inhibitor, a_1-antitrypsin (Heeb *et al.*, 1990, *J. Biol. Chem.* 265 : 2365-2369; Schapira *et al.*, 1987, *J. Clin. Invest.* 80:582-585). The peptides and peptide mimetics comprise the sequence Arg-Xaa-Xaa-Arg (SEQ ID No. 4) or peptido-, organo- or chemical mimetics thereof.

The invention provides methods for inhibiting bacterial infection of human cells comprising contacting such cells with an effective amount of a peptide or peptide mimetic of the invention. In a preferred embodiment, the bacterial infection is caused by *Corynebacterium diptheriae*. In another preferred embodiment, the bacterial

infection is caused by *Bacillus anthracis*. In yet another preferred embodiment, the bacterial infection is caused by *Pseudomonas aeruginosa*.

The invention also provides a method of inhibiting bacterial infection in a human comprising administering a therapeutically effective amount of a peptide or peptide mimetic of the invention in a pharmaceutically acceptable carrier. In a preferred embodiment, the bacterial infection is caused by *Corynebacterium diptheriae*. In another preferred embodiment, that bacterial is caused by *Bacillus anthracis*. In yet another preferred embodiment, the bacterial infection is caused by *Pseudomonas aeruginosa*.

Another method provided by the invention for treating humans with a bacterial infection comprises administering a combination of a therapeutically effective amount of a peptide or peptide mimetic of the invention and a therapeutically effective amount of a second antibacterial compound in a pharmaceutically acceptable carrier. In a preferred embodiment, the bacterial infection is caused by *Corynebacterium diptheriae*. In another preferred embodiment, the bacterial infection is caused by *Bacillus anthracis*. In yet another preferred embodiment, the bacterial infection is caused by *Pseudomonas aeruginosa*.

Pharmaceutically acceptable compositions effective according to the methods of the invention, comprising a therapeutically effective amount of a peptide or peptide mimetic of the invention capable of blocking endoproteolytic activation of bacterial toxins and a pharmaceutically acceptable carrier or diluent, are also provided.

The invention provides a method of inhibiting viral infection of human cells comprising contacting such cells with an effective amount of a peptide or peptide mimetic of the invention. In preferred embodiments, the viral infection is caused by human cytomegalovirus (HCMV), yellow fever virus, measles virus, mumps virus, influenza virus, varicella zooster virus, or human immunodeficiency virus (HIV-1). In another preferred embodiment, the human cells are hematopoietic cells, most preferably T lymphocytes.

The invention also provides a method for inhibiting viral infection in an animal, most preferably a human, comprising administering a therapeutically effective amount of a peptide or peptide mimetic of the invention in a pharmaceutically acceptable carrier. In preferred embodiments, the viral infection is caused by human cytomegalovirus,

yellow fever virus, measles virus, mumps virus, influenza virus, varicella zooster virus, or human immunodeficiency virus.

The invention provides a method of treating humans infected with a virus comprising administering a therapeutically effective amount of a peptide or peptide mimetic of the invention in a pharmaceutically acceptable carrier. In preferred embodiments, the viral infection is caused by human cytomegalovirus, yellow fever virus, measles virus, mumps virus, influenza virus, varicella zooster virus, or human immunodeficiency virus.

The invention provides a method of treating humans infected with a virus comprising administering a combination of a therapeutically effective amount of a peptide or peptide mimetic of the invention and a therapeutically effective amount of a second antiviral compound in a pharmaceutically acceptable carrier. In preferred embodiment, the virus is HIV-1 and the second antiviral compound is azidothymidine. In another preferred embodiment, the virus is HCMV and the second antiviral compound is foscarnet, gancyclovir, or cidofovir.

Pharmaceutically acceptable compositions effective according to the methods of the invention, comprising a therapeutically effective amount of a peptide or peptide mimetic of the invention having antiviral properties and a pharmaceutically acceptable carrier or diluent, are also provided.

The invention also provides a method of inhibiting proteolytic processing of a biologically active protein or peptide in a cell comprising contacting such cells with a peptide or peptide mimetic of the invention. Preferred biologically active proteins are pro-β-nerve growth factor, blood coagulation factor protein Factor IX, pro-von Willibrand factor, complement factor C3 and renin.

Specific preferred embodiments of the present invention will become evident from the following more detailed description of certain preferred embodiments and the claims.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1A is a computer generated molecular model of the reactive site loop (RSL) portion of the α_1-antitrypsin Portland (PDX) variant comprising the sequence - Arg_{355}-Ile_{356}-Pro_{357}-Arg_{358}- (SEQ ID No. 3). Figure 1A shows a view in which certain

atoms in the peptide backbone and arginine sidechains have been numbered. Figure 1B shows rotated views from six perspectives of the molecule.

Figure 2 shows the structure of *Pseudomonas aeruginosa* pro-exotoxin A (PEA) and human cytomegalovirus pro-gB (HCMV progB) proteins, including the furin recognition site.

Figure 3 sets forth a schematic diagram of an assay using detection of *P. aeruginosa* exotoxin A-mediated cellular protein synthesis inhibition to detect compounds that inhibit furin-mediated maturation of the exotoxin.

Figure 4 is a graph of the results of the assay described in Example 1 and performed according to the protocol set forth in Figure 3.

Figure 5 is a diagram of the cleavage pattern of HCMV pro-gB protein.

Figure 6 sets forth a schematic diagram of an assay using detection of plaque formation in naive human foreskin fibroblasts (HFF) incubated with the supernatant fluid of an HCMV-infected culture of U373 cells in the presence or absence of a putative furin inhibiting compound.

Figure 7 is a graph of the results of a plaque-forming assay described in Example 1 and performed according to the protocol set forth in Figure 6.

Figure 8 is a Western blot of proteins produced by HCMV-infected U373 cells and probed with a gB-specific antibody.

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

For the purposes of this invention, the terms "mimetic," "peptide mimetic," "peptidomimetic," "organomimetic" and "chemical mimetic" are intended to encompass peptide derivatives, peptide analogues and chemical compounds having an arrangement of atoms is a three-dimensional orientation that is equivalent to that of a peptide having the sequence Arg-Xaa-Xaa-Arg (SEQ ID No.: 4). It will be understood that the phrase "equivalent to" as used herein is intended to encompass compounds having substitution of certain atoms or chemical moieties in said peptide with moieties having bond lengths, bond angles and arrangements thereof in the mimetic compound that produce the same or sufficiently similar arrangement or orientation of said atoms and moieties to have the biological function of inhibiting furin endoprotease activity. In the peptide mimetics of the invention, the three-dimensional arrangement of the chemical constituents is

structurally and/or functionally equivalent to the three-dimensional arrangement of the peptide backbone and component amino acid sidechains in the peptide, resulting in such peptido-, organo- and chemical mimetics of the peptides of this invention having substantial biological activity, specifically furin protease inhibiting activity. These terms are used according to the understanding in the art, as illustrated *for example* by Fauchere, 1986, *Adv. Drug Res.* 15: 29; Veber & Freidinger, 1985, *TINS* p.392; and Evans et al., 1987, *J. Med. Chem.* 30: 1229, incorporated herein by reference.

It is understood that a pharmacophore exists for the biological activity of the PDX protein of the invention, said pharmacophore being defined by the -Arg-Xaa-Xaa-Arg- (SEQ ID No. 4) portion of the PDX protein at residues 355-358. A pharmacophore is understood in the art as comprising an idealized, three-dimensional definition of the structural requirements for biological activity. The determination of the three-dimensional structure of the PDX protein provides the structural information to enable production of peptido-, organo- and chemical mimetics of the functional portion of PDX. Peptido-, organo- and chemical mimetics can be designed to fit each pharmacophore with current computer modeling software (computer aided drug design), as described in more detail below. Said mimetics are produced by structure-function analysis, based on the positional information from the crystallographic-derived molecular positional information disclosed herein.

In a first embodiment, the invention provides peptides defined by the sequence Arg-Xaa-Xaa-Arg. In a preferred embodiment, the peptides of the invention have the sequence Arg-Xaa-Pro-Arg (SEQ ID No. 5). In additional preferred embodiments, the peptide comprises the sequence Arg-Ile-Pro-Arg (SEQ ID No. 4). It will be understood that the use of "Xaa" for these residues is intended to indicate that any amino acid residue can be substituted for Ile or Pro in these positions with no change in the critical dimensions of the rigid reactive site loop (RSL) of the PDX protein, as disclosed herein. Peptide analogues of the invention include embodiments whereby either of the arginine residues are substituted by positively-charged amino acids including lysine, homolysine, hydroxylysine, ornithine, citrulline and canavanine. In preferred embodiments, both arginine residues are substituted by the same alternative amino acid.

Alternative embodiments of the peptides of the invention include peptides having the sequence B-(Arg-Xaa-Xaa-Arg)-C, wherein "B" and "C" represent amino acid sequences each independently comprising from about 1 to about 40 amino acids, more

preferably from about 5 to about 30 amino acids and most preferably from about 10 to about 25 amino acid residues. In particularly preferred embodiments, the B-(Arg-Xaa-Xaa-Arg)-C peptides of the invention are conformationally-restricted, *for example* by cyclization or disulfide bond formation, wherein the term "disulfide bond" is intended to encompass sulfide linkages and other disulfide derivatives, particularly those that are more stable than naturally-occurring disulfide bonds. In additional preferred embodiments, the peptides of the invention are derivatized by attachment of sugar moieties to produce glycosylated analogues thereof, wherein the sugar moieties are covalently linked to an asparagine residue ("N-linked" glycosylation) or serine, hydroxyproline, hydroxylysine, or threonine residues ("O-linked" glycosylation). Peptides wherein either the amino or carboxyl termini are derivitized are also within the scope of the peptides of the invention.

Conjugation with sugars (preferably glucose, glucosamine, galactose, galactosamine, mannose, mannosamine, maltose and the like) at the – or C-terminus, at internal asparagine, serine or threonine residues, or at the N-terminus by means of a succinyl linker, serves to stabilize certain conformational motifs, and may increase solubility and bioavailability of the peptide. Similarly, polyethylene glycol (PEG) conjugation at – or C-terminus or on side chains can stabilize peptides and improve pharmacological performance (*see, for example,* Delgado *et al.*, 1992, *Crit. Rev. Ther. Drug Carrier Syst.* 9: 249-304). Such modifications may change the *in vitro* profile of a mimetic, and enhance circulating half-life and *in vivo* activity.

Peptides as provided by the invention may be advantageously synthesized by any of the chemical synthesis techniques known in the art, particularly solid-phase synthesis techniques, *for example*, using commercially-available automated peptide synthesizers. The mimetics of the present invention can be synthesized by solid phase or solution phase methods conventionally used for the synthesis of peptides (*see, for example*, Merrifield, 1963, *J. Amer. Chem. Soc.* 85: 2149-54; Carpino, 1973, *Acc. Chem. Res.* 6: 191-98; Birr, 1978, ASPECTS OF THE MERRIFIELD PEPTIDE SYNTHESIS, Springer-Verlag: Heidelberg; THE PEPTIDES: ANALYSIS, SYNTHESIS, BIOLOGY, Vols. 1, 2, 3, 5, (Gross & Meinhofer, eds.), Academic Press: New York, 1979; Stewart *et al.*, 1984, SOLID PHASE PEPTIDE SYNTHESIS, 2d. ed., Pierce Chem. Co.: Rockford, Ill.; Kent, 1988, *Ann. Rev. Biochem.* 57: 957-89; and Gregg *et al.*, 1990, *Int. J. Peptide Protein Res.* 55: 161-214 , which are incorporated herein by reference in their entirety.)

The use of solid phase methodology is preferred. Briefly, an N-protected C-terminal amino acid residue is linked to an insoluble support such as divinylbenzene cross-linked polystyrene, polyacrylamide resin, Kieselguhr/polyamide (pepsyn K), controlled pore glass, cellulose, polypropylene membranes, acrylic acid-coated polyethylene rods or the like. Cycles of deprotection, neutralization and coupling of successive protected amino acid derivatives are used to link the amino acids from the C-terminus according to the amino acid sequence. For some synthetic peptides, an Fmoc strategy using an acid-sensitive resin may be used. Preferred solid supports in this regard are divinylbenzene cross-linked polystyrene resins, which are commercially available in a variety of functionalized forms, including chloromethyl resin, hydroxymethyl resin, paraacetamidomethyl resin, benzhydrylamine (BHA) resin, 4-methylbenzhydrylamine (MBHA) resin, oxime resins, 4-alkoxybenzyl alcohol resin (Wang resin), 4-(2',4'-dimethoxyphenylaminomethyl)-phenoxymethyl resin, 2,4-dimethoxybenzhydrylamine resin, and 4-(2',4'-dimethoxyphenyl-FMOC-aminomethyl)-phenoxyacetamidonorleucyl-MBHA resin (Rink amide MBHA resin). In addition, acid-sensitive resins also provide C-terminal acids, if desired.

A particularly preferred protecting group for alpha. amino acids is base-labile 9-fluorenylmethoxycarbonyl (Fmoc). Suitable protecting groups for the side chain functionalities of amino acids chemically compatible with Boc (t-butyloxycarbonyl) and Fmoc groups are well known in the art. When using Fmoc chemistry, the following protected amino acid derivatives are preferred: Fmoc-Cys(Trit), Fmoc-Ser(But), Fmoc-Asn(Trit), Fmoc-Leu, Fmoc-Thr(Trit), Fmoc-Val, Fmoc-Gly, Fmoc-Lys(Boc), Fmoc-Gln(Trit), Fmoc-Glu(OBut), Fmoc-His(Trit), Fmoc-Tyr(But), Fmoc-Arg(PMC(=2,2,5,7,8-pentamethylchroman-6-sulfonyl)), Fmoc-Arg(Boc)$_2$, Fmoc-Pro, and Fmoc-Trp(Boc). The amino acid residues can be coupled by using a variety of coupling agents and chemistries known in the art, such as direct coupling with DIC (diisopropyl-carbodiimide), DCC (dicyclohexylcarbodiimide), BOP (benzotriazolyl-N-oxytrisdimethylaminophosphonium hexa-fluorophosphate), PyBOP (benzotriazole-1-yl-oxy-tris-pyrrolidinophosphonium hexafluoro-phosphate), or PyBrOP (bromo-tris-pyrrolidinophosphonium hexafluorophosphate); *via* preformed symmetrical anhydrides; *via* active esters such as pentafluorophenyl esters; *via* performed HOBt (1-hydroxybenzotriazole) active esters; by using Fmoc-amino acid fluoride and chlorides; or by using Fmoc-amino acid-N-carboxy anhydrides. Activation with HBTU (2-(1H-

benzotriazole-1-yl)-1,1,3,3-tetramethyluronium hexafluorophosphate) or HATU (2-(1H-7-aza-benzotriazole-1-yl)-(1,1,3,3-tetramethyluronium hexafluorophosphate) in the presence of HOBt or HOAt (7-azahydroxybenztriazole) is preferred.

Solid phase methods can be carried out manually, although automated synthesis on a commercially available peptide synthesizer (*e.g.*, Applied Biosystems 431A or the like; Applied Biosystems, Foster City, CA) is preferred. In a typical synthesis, the first (C-terminal) amino acid is loaded on the chlorotrityl resin. Successive deprotection (with 20% piperidine/NMP (N-methylpyrrolidone)) and coupling cycles according to ABI FastMoc protocols (ABI user bulletins 32 and 33, Applied Biosystems) are used to build the complete peptide sequence. Double and triple coupling, with capping by acetic anhydride, may also be used.

The synthetic mimetic peptide is advantageously cleaved from the resin and deprotected by treatment with TFA (trifluoroacetic acid) containing appropriate scavengers. Many such cleavage reagents, such as Reagent K (0.75 g crystalline phenol/ 0.25 mL ethanedithiol/ 0.5 mL thioanisole/ 0.5 mL deionized water/ 10 mL TFA), can be used. The peptide is separated from the resin by filtration and isolated by ether precipitation. Further purification may be achieved by conventional methods, such as gel filtration and reverse phase HPLC (high performance liquid chromatography). Synthetic mimetics according to the present invention may be in the form of pharmaceutically acceptable salts, especially base-addition salts and including salts of organic bases and inorganic bases. The base-addition salts of the acidic amino acid residues are prepared by treatment of the peptide with the appropriate base, according to procedures well known to those skilled in the art, or the desired salt may be obtained directly by lyophilization out of the appropriate base solution.

Generally, those skilled in the art will recognize that peptides as described herein may be modified by a variety of chemical techniques to produce compounds having essentially the same activity as the unmodified peptide, and optionally having other desirable properties. For example, carboxylic acid groups of the peptide may be provided in the form of a salt of a pharmaceutically-acceptable cation. Amino groups within the peptide may be in the form of a pharmaceutically-acceptable acid addition salt, such as the HCl, HBr, acetic, benzoic, toluene sulfonic, maleic, tartaric and other organic salts, or may be converted to an amide. Thiols can be protected with any one of a number of well-recognized protecting groups, such as acetamide groups. Those

skilled in the art will also recognize methods for introducing cyclic structures into the peptides of this invention so that the native binding configuration will be more nearly approximated. For example, a carboxyl terminal or amino terminal cysteine residue can be added to the peptide, so that when oxidized the peptide will contain a disulfide bond, thereby generating a cyclic peptide. Other peptide cyclizing methods include the formation of thioethers and carboxyl- and amino-terminal amides and esters.

Specifically, a variety of techniques are available for constructing peptide derivatives and analogues with the same or similar desired biological activity as the corresponding peptide compound but with more favorable activity than the peptide with respect to solubility, stability, and susceptibility to hydrolysis and proteolysis. Such derivatives and analogues include peptides modified at the N-terminal amino group, the C-terminal carboxyl group, and/or changing one or more of the amido linkages in the peptide to a non-amido linkage. It will be understood that two or more such modifications can be coupled in one peptide mimetic structure (*e.g.*, modification at the C-terminal carboxyl group and inclusion of a $-CH_2-$ carbamate linkage between two amino acids in the peptide, *for example*).

Amino terminus modifications include but are not limited to alkylating, acetylating, adding a carbobenzoyl group, and forming a succinimide group. Specifically, the N-terminal amino group can be reacted to form an amide group of the formula RC(O)NH-, where R is alkyl, preferably lower alkyl, and is added by reaction with an acid halide or acid anhydride. Typically, the reaction can be conducted by contacting about equimolar or excess amounts (*e.g.*, about 5 equivalents) of an acid halide to the peptide in an inert diluent (*e.g.*, dichloromethane) preferably containing an excess (*e.g.*, about 10 equivalents) of a tertiary amine, such as diisopropylethylamine, to scavenge the acid generated during reaction. Reaction conditions are otherwise conventional (*e.g.*, room temperature for 30 minutes). Alkylation of the terminal amino to provide for a lower alkyl N-substitution followed by reaction with an acid halide as described above will provide for N-alkyl amide group of the formula RC(O)NR–.

Alternatively, the amino terminus can be covalently linked to succinimide group by reaction with succinic anhydride. An approximately equimolar amount or an excess of succinic anhydride (*e.g.*, about 5 equivalents) are used and the terminal amino group is converted to the succinimide by methods well known in the art including the use of an excess (*e.g.*, ten equivalents) of a tertiary amine such as diisopropylethylamine in a

suitable inert solvent (*e.g.*, dichloromethane), as described in Wollenberg et al., U.S. Pat. No. 4,612,132 which is incorporated herein by reference in its entirety. It will also be understood that the succinic group can be substituted with, for example, C_2- through C_6- (*i.e.*, lower) alkyl or --SR substituents (where R is alkyl, preferably lower alkyl), which are prepared in a conventional manner to provide for substituted succinimide at the N-terminus of the peptide. Such alkyl substituents are prepared by reaction of a lower olefin (C_2- through C_6- alkyl) with maleic anhydride in the manner described by Wollenberg *et al.*, *supra.*, and --SR substituents are prepared by reaction of RSH with maleic anhydride. In other advantageous embodiments, the amino terminus is derivatized to form a benzyloxycarbonyl-NH-- or a substituted benzyloxycarbonyl-NH-- group. This derivative is produced by reaction with approximately an equivalent amount or an excess of benzyloxycarbonyl chloride (CBZ-Cl) or a substituted CBZ-Cl in a suitable inert diluent (*e.g.*, dichloromethane) preferably containing a tertiary amine to scavenge the acid generated during the reaction. In yet another derivative, the N-terminus comprises a sulfonamide group by reaction with an equivalent amount or an excess (*e.g.*, 5 equivalents) of R-$S(O)_2Cl$ in a suitable inert diluent (dichloromethane) to convert the terminal amine into a sulfonamide, where R is alkyl and preferably lower alkyl. Preferably, the inert diluent contains excess tertiary amine (*e.g.*, 10 equivalents) such as diisopropylethylamine, to scavenge the acid generated during reaction. Reaction conditions are otherwise conventional as described above. Carbamate groups are produced at the amino terminus by reaction with an equivalent amount or an excess (*e.g.*, 5 equivalents) of ROC(O)Cl or R-$OC(O)OC_6H_4$-*p*-NO_2 in a suitable inert diluent (*e.g.*, dichloromethane) to convert the terminal amine into a carbamate, where R is alkyl, preferably lower alkyl. Preferably, the inert diluent contains an excess (*e.g.*, about 10 equivalents) of a tertiary amine, such as diisopropylethylamine, to scavenge any acid generated during reaction. Reaction conditions are otherwise conventional as described above. Urea groups are formed at the amino terminus by reaction with an equivalent amount or an excess (*e.g.*, 5 equivalents) of RN=C=O in a suitable inert diluent (*e.g.*, dichloromethane) to convert the terminal amine into a urea (*i.e.*, RNHC(O)NH--) group where R is as defined above. Preferably, the inert diluent contains an excess (e.g., about 10 equivalents) of a tertiary amine, such as diisopropylethylamine. Reaction conditions are otherwise conventional as described above.

In preparing peptide mimetics wherein the C-terminal carboxyl group is replaced

by an ester (*e.g.*, -C(O)OR where R is alkyl and preferably lower alkyl), resins used to prepare the peptide acids are employed, and the side chain protected peptide is cleaved with base and the appropriate alcohol, *e.g.*, methanol. Side chain protecting groups are then removed in the usual fashion by treatment with hydrogen fluoride to obtain the desired ester. In preparing peptide mimetics wherein the C-terminal carboxyl group is replaced by the amide -C(O)NR_3R_4, a benzhydrylamine resin is used as the solid support for peptide synthesis, wherein R_3 and R_4 are independently alkyl, most preferably lower alkyl. Upon completion of synthesis, hydrogen fluoride treatment to release the peptide from the support results directly in the free peptide amide (*i.e.*, the C-terminus is -C(O)NH_2). Alternatively, use of chloromethylated resin during peptide synthesis coupled with reaction with ammonia to cleave the side chain protected peptide from the support yields the free peptide amide, and reaction with an alkylamine or a dialkylamine yields a side chain protected alkylamide or dialkylamide (*i.e.*, the C-terminus is -C(O)NRR_1, where R and R_1 are independently alkyl and preferably lower alkyl). Side chain protection is then removed in the usual fashion by treatment with hydrogen fluoride to give the free amides, alkylamides, or dialkylamides.

In another alternative embodiment, the C-terminal carboxyl group or a C-terminal ester can be induced to cyclize by displacement of the -OH or the ester (-OR) of the carboxyl group or ester, respectively, with the N-terminal amino group to form a cyclic peptide. For example, after synthesis and cleavage to give the peptide acid, the free acid is converted in solution to an activated ester by an appropriate carboxyl group activator such as dicyclohexylcarbodiimide (DCC), *for example*, in methylene chloride (CH_2Cl_2), dimethyl formamide (DMF), or mixtures thereof. The cyclic peptide is then formed by displacement of the activated ester with the N-terminal amine. Cyclization, rather than polymerization, can be enhanced by use of very dilute solutions according to methods well known in the art.

Peptide mimetics as understood in the art and provided by the invention are structurally similar to the paradigm polypeptide comprising the sequence Arg-Xaa-Xaa-Arg (SEQ ID No. 2), but have one or more peptide linkages optionally replaced by a linkage selected from the group consisting of: --CH_2NH--, --CH_2S--, --CH_2CH_2 --, --CH=CH– (in both *cis* and *trans* conformers), --$COCH_2$--, --CH(OH)CH_2 --, and --CH_2SO--, by methods known in the art and further described in the following references: Spatola,1983, *in* CHEMISTRY AND BIOCHEMISTRY OF AMINO ACIDS, PEPTIDES, AND

PROTEINS, (Weinstein, ed.), Marcel Dekker: New York, p. 267; Spatola, 1983, *Peptide Backbone Modifications* 1: 3; Morley, 1980, *Trends Pharm. Sci.* pp. 463-468; Hudson *et al.*, 1979, *Int. J. Pept. Prot. Res.* 14: 177-185; Spatola *et al.*, 1986, *Life Sci.* 38: 1243-1249; Hann, 1982, *J. Chem. Soc. Perkin Trans.* I 307-314; Almquist *et al.*, 1980, *J. Med. Chem.* 23: 1392-1398; Jennings-White *et al.*, 1982, *Tetrahedron Lett.* 23: 2533; Szelke *et al.*, 1982, European Patent Application, Publication No. EP045665A; Holladay *et al.*, 1983, *Tetrahedron Lett.* 24: 4401-4404; and Hruby, 1982, *Life Sci.* 31: 189-199, each of which is incorporated herein by reference. Such peptide mimetics may have significant advantages over polypeptide embodiments, including, for example: being more economical to produce, having greater chemical stability or enhanced pharmacological properties (such half-life, absorption, potency, efficacy, etc.), reduced antigenicity, and other properties.

The invention also provides a detailed structural determination of the reactive site loop (RSL) of the PDX protein. The importance of this structure determination, *inter alia*, relates to the determination that this structure, the RSL, forms a rigid backbone having the positively-charged guanidino residues of each of the Arg residues extending in space away in the same direction from the rest of the PDX protein. This determination results in the capacity to produce peptido-, organo- and chemical mimetics of this portion of the PDX protein structure, said mimetics being capable of inhibiting furin protease activity.

In a second embodiment, the invention provides organic molecules designed to mimic the peptides of the invention by having chemically-similar atoms, moieties or collections thereof in positions analogous to the positions of the atoms, moieties and collections thereof in the Arg-Xaa-Xaa-Arg-comprising peptides of the invention. In a preferred embodiment, these mimetic compounds have the structure:

C(L1-R1)-E-F-G-H-I-J(L2-R2)

wherein "C" is equivalent to the alpha carbon of the first arginine residue, and "J" is equivalent to the alpha carbon of the second arginine residue, in the Arg-Xaa-Xaa-Arg-containing peptides of the invention. Most preferably, "C" and "J" are conformationally hindered as described herein to enable the mimetic to stably adopt the configuration for the (L1-R1) and (L2-R2) substituents present in the Arg-Xaa-Xaa-Arg-containing

peptides of the invention. "E", "G", and "I" represent planar moieties having dimensions similar to those of a peptide bond (as disclosed in Metzler, 1977, BIOCHEMISTRY: THE CHEMICAL REACTIONS OF LIVING CELLS, Academic Press: New York, p.64). Non-limiting examples of such moieties include vinyl groups and substituted vinyl groups. "F" and "H" are equivalent to the alpha carbons of the two "Xaa" residues in the peptides of the invention, and are preferably conformationally-hindered, *for example*, by having "H" be restricted in a cyclopentane, cyclopentene, furan, tetrahydrofuran, thiophene, pyrrole, or pyrrolidine ring structure, or by covalent linkage to sterically-hindered groups, such as *t*-butyl, phenyl, benzyl or substituted phenyl or benzyl groups. The structure represented by E-F-G-H-I is most preferably substantially planar and deviates from this planar structure (*for example*, by bending, defined herein as flexion above or below the plane defined by E-F-G-H-I) by no more than from about 1 to about 20 degrees, more preferably from about 1 to about 10 degrees, and most preferably by no more than about 5 degrees from said plane. The length of the molecule along the distance between the "C" and "J" components (C-E-F-G-H-I-J) is preferably from about 7.5 to about 11.5 Angstroms, more preferably from about 8.5 to about 10.5 Angstroms, and most preferably about 9.5 Angstroms. R1 and R2 are positively-charged residues linked to "C" and "J", respectively, by linker groups L1 and L2, respectively, wherein the distance between "C" and L1 and the distance between "J" and L2 is substantially equivalent to the distances between the alpha carbon atoms and the guanidino groups of each of the arginine residues in the Arg-Xaa-Xaa-Arg-containing peptides of the invention. Preferably, R1 and R2 are from about 5 to about 7 Angstroms, more preferably from about 5.6 to about 6.7 Angstroms, and most preferably about 6.2 Angstroms away from their respective alpha carbon equivalents, "C" and "J", and the length of L1 and L2 is chosen to maintain this relative positioning in the mimetic molecule. In addition, R1 and R2 are displaced relative to each other along the longitudinal axis of the molecule to subtend an angle of from about 15 to about 25 degrees, more preferably from about 18 to about 21 degrees, and most preferably about 20 degrees. This arrangement is illustrated in Figure 1B, *Left* and *Right*, where the arginine sidechains of both arginine residues in the Arg-Ile-Pro-Arg pharmacophore of the preferred peptide of the invention are shown in orange and red.

The invention provides a pharmacophore for the reactive site loop of the α_1-antitrypsin variant Portland (SEQ ID No. 1) defined by the sequence Arg_{355}-Ile_{356}-Pro_{357}-

Arg_{358} in this protein. This pharmacophore is represented in Figure 1A, wherein the atom designated "3" is the alpha carbon atom of Arg_{355}, and the atom designated "12" is the alpha carbon atom of Arg_{358}. These values were derived from the analysis of the crystal structure of the Portland protein as generated by the SYBYL® program (Tripos, Inc., St. Louis, MO); the complete structural information used in these analyses is contained in Appendix A disclosed herewith. The specific portion of these data relating to the sequence Arg_{355}-Ile_{356}-Pro_{357}-Arg_{358} is as follows:

ATOM	2635	N	ARG	355	-21.632	17.983	16.258	1.00	29.44
ATOM	2636	CA	ARG	355	-23.045	18.139	16.553	1.00	28.26
ATOM	2637	C	ARG	355	-23.749	16.840	16.270	1.00	30.07
ATOM	2638	O	ARG	355	-24.289	16.646	15.192	1.00	31.20
ATOM	2639	CB	ARG	355	-23.609	19.272	15.673	1.00	0.00
ATOM	2640	CG	ARG	355	-22.959	20.610	16.072	1.00	0.00
ATOM	2641	CD	ARG	355	-23.486	21.721	15.145	1.00	0.00
ATOM	2642	NE	ARG	355	-22.825	22.976	15.457	1.00	0.00
ATOM	2643	CZ	ARG	355	-23.124	24.073	14.823	1.00	0.00
ATOM	2644	NH1	ARG	355	-24.026	24.089	13.887	1.00	0.00
ATOM	2645	NH2	ARG	355	-22.507	25.176	15.134	1.00	0.00
ATOM	2646	N	ILE	356	-23.743	15.932	17.265	1.00	21.27
ATOM	2647	CA	ILE	356	-24.424	14.667	17.057	1.00	19.01
ATOM	2648	C	ILE	356	-25.898	14.821	17.330	1.00	26.05
ATOM	2649	O	ILE	356	-26.268	15.297	18.392	1.00	26.38
ATOM	2650	CB	ILE	356	-23.787	13.551	17.907	1.00	20.54
ATOM	2651	CG1	ILE	356	-22.307	13.409	17.503	1.00	19.50
ATOM	2652	CG2	ILE	356	-24.521	12.219	17.649	1.00	21.25
ATOM	2653	CD1	ILE	356	-21.595	12.415	18.434	1.00	17.49
ATOM	2654	N	PRO	357	-26.758	14.439	16.364	1.00	24.53
ATOM	2655	CA	PRO	357	-28.188	14.615	16.534	1.00	24.80
ATOM	2656	C	PRO	357	-28.782	13.579	17.447	1.00	33.18
ATOM	2657	O	PRO	357	-28.209	12.517	17.631	1.00	34.40
ATOM	2658	CB	PRO	357	-28.715	14.367	15.106	1.00	25.84
ATOM	2659	CG	PRO	357	-27.572	13.703	14.306	1.00	29.85
ATOM	2660	CD	PRO	357	-26.275	13.877	15.121	1.00	24.59
ATOM	2661	N	ARG	358	-29.953	13.908	18.026	1.00	31.16
ATOM	2662	CA	ARG	358	-30.616	12.936	18.877	1.00	30.88
ATOM	2663	C	ARG	358	-31.428	12.004	18.024	1.00	31.32
ATOM	2664	O	ARG	358	-32.569	12.288	17.695	1.00	31.76
ATOM	2665	CB	ARG	358	-31.466	13.637	19.957	1.00	0.00
ATOM	2666	CG	ARG	358	-32.415	14.682	19.338	1.00	0.00
ATOM	2667	CD	ARG	358	-33.096	15.460	20.478	1.00	0.00
ATOM	2668	NE	ARG	358	-34.540	15.347	20.380	1.00	0.00
ATOM	2669	CZ	ARG	358	-35.327	16.130	21.061	1.00	0.00
ATOM	2670	NH1	ARG	358	-34.853	17.034	21.867	1.00	0.00
ATOM	2671	NH2	ARG	358	-36.616	16.007	20.933	1.00	0.00

wherein "ATOM" indicates the number of the atom in the analyzed sequence, the residue number is shown in column 5, the chemical identity of the residue at each position is shown in column 4, and the analyzed atom is shown in column 3. In column 3, "N" is a peptide nitrogen, "CA" is the alpha carbon, "C" is the peptide carbonyl carbon, "O" is the peptide carbonyl oxygen, "CB", "CG", and "CD" are sidechain methyl or methylene carbon atoms, "NE" is the imino nitrogen of the guanidino group of arginine, "CZ" is the carbon atom of the guanidino group of arginine, and "NH1" and "NH2" are the amino nitrogen atoms of the guanidino group of arginine. Columns 6, 7 and 8 represent the positional information of each atom in the x, y and z axes, respectively. These aspects of the invention are further illustrated in Figure 1B, which shows perspective views of the SYBYL model of the RSL of PDX.

The positional information relating the atoms in this structure is shown in Tables I, II and III:

TABLE I

Atom Number	Angle (degrees)
1-2-3	31.64
2-3-3.1	36.93
2-3-4	36.26
3.1-3-4	35.05
3-4-5	29.95
4-5-6	31.94
5-6-7	35.69
6-7-8	29.22
7-8-9	30.85
8-9-10	30.1
9-10-11	31.75
10-11-12	36.07
11-12-12.1	35.72
11-12-13	30.48
12-12.1-13	34.3

TABLE II

Atoms	Distance (Angstroms)
3-3.5	6.18
12-12.5	6.1
3-12	9.48

TABLE III

Atom	Degrees		
	W	φ (phi)	ψ (psi)
3	-178.5	-87	85.29
6	179.09	82.73	126
9	-177.2	-76.9	157.9
12	177.45	-76.9	157.9

The complete positional data for the PDX protein is disclosed herein in Appendix A.

Mimetic analogs of the Arg-Xaa-Xaa-Arg-containing peptides of the invention may also be obtained using the principles of conventional or rational drug design (*see*, Andrews *et al.*, 1990, *Proc. Alfred Benzon Symp.* 28: 145-165; McPherson, 1990, *Eur. J. Biochem.* 189:1-24; Hol *et al.*, 1989a, *in* MOLECULAR RECOGNITION: CHEMICAL AND BIOCHEMICAL PROBLEMS, (Roberts, ed.), Royal Society of Chemistry; pp. 84-93; Hol, 1989b, *Arzneim-Forsch.* 39:1016-1018; Hol, 1986, *Agnew Chem. Int. Ed. Engl.* 25: 767-778, the disclosures of which are herein incorporated by reference).

In accordance with the methods of conventional drug design, the desired mimetic molecules are obtained by randomly testing molecules whose structures have an attribute in common with the structure of a "native" Arg-Xaa-Xaa-Arg peptide. The quantitative contribution that results from a change in a particular group of a binding molecule can be determined by measuring the biological activity of the putative mimetic (furin-inhibiting activity) in comparison with the furin-inhibiting activity of the Arg-Xaa-Xaa-Arg-containing peptide. In a preferred embodiment of rational drug design, the mimetic is designed to share an attribute of the most stable three-dimensional conformation of

the Arg-Xaa-Xaa-Arg peptide. Thus, for example, the mimetic may be designed to possess chemical groups that are oriented in a way sufficient to cause ionic, hydrophobic, or van der Waals interactions that are similar to those exhibited by the furin-inhibiting peptides of the invention, as disclosed herein.

The preferred method for performing rational mimetic design employs a computer system capable of forming a representation of the three-dimensional structure of the Arg-Xaa-Xaa-Arg-containing peptide, such as those exemplified by Hol, 1989a, *ibid.*; Hol, 1989b, *ibid.*; and Hol, 1986, *ibid.* Molecular structures of the peptido-, organo- and chemical mimetics of the peptides of the invention are produced according to those with skill in the art using computer-assisted design programs commercially available in the art. Examples of such programs include SYBYL 6.5®, HQSAR™, and ALCHEMY 2000™ (Tripos); GALAXY™ and AM2000™ (AM Technologies, Inc., San Antonio, TX); CATALYST™ and CERIUS™ (Molecular Simulations, Inc., San Diego, CA); CACHE PRODUCTS™, TSAR™, AMBER™, and CHEM-X™ (Oxford Molecular Products, Oxford, CA) and CHEMBUILDER3D™ (Interactive Simulations, Inc., San Diego, CA).

The peptido-, organo- and chemical mimetics produced using the positional information disclosed herein using, for example, art-recognized molecular modeling programs are produced using conventional chemical synthetic techniques, most preferably designed to accommodate high throughput screening, including combinatorial chemistry methods. Combinatorial methods useful in the production of the peptido-, organo- and chemical mimetics of the invention include phage display arrays, solid-phase synthesis and combinatorial chemistry arrays, as provided, for example, by SIDDCO, Tucson, Arizona; Tripos, Inc.; Calbiochem/Novabiochem, San Diego, CA; Symyx Technologies, Inc., Santa Clara, CA; Medichem Research, Inc., Lemont, IL; Pharm-Eco Laboratories, Inc., Bethlehem, PA; or N.V. Organon, Oss, Netherlands. Combinatorial chemistry production of the peptido-, organo- and chemical mimetics of the invention are produced according to methods known in the art, including but not limited to techniques disclosed in Terrett, 1998, COMBINATORIAL CHEMISTRY, Oxford University Press, London; Gallop *et al.*, 1994, "Applications of combinatorial technologies to drug discovery. 1. Background and peptide combinatorial libraries," *J. Med. Chem.* 37: 1233-51; Gordon *et al.*, 1994, "Applications of combinatorial technologies to drug discovery. 2. Combinatorial organic synthesis, library screening strategies, and future directions," *J. Med. Chem.* 37: 1385-1401; Look *et al.*, 1996,

Bioorg. Med. Chem. Lett. 6: 707-12; Ruhland *et al.*, 1996, *J. Amer. Chem. Soc.* 118: 253-4; Gordon *et al.*, 1996, *Acc.Chem. Res.* 29: 144-54; Thompson & Ellman, 1996, *Chem. Rev.* 96: 555-600; Fruchtel & Jung, 1996, *Angew. Chem. Int. Ed. Engl.* 35: 17-42; Pavia, 1995, "The Chemical Generation of Molecular Diversity", Network Science Center, www.netsci.org; Adnan *et al.*, 1995, "Solid Support Combinatorial Chemistry in Lead Discovery and SAR Optimization," *Id.*, Davies and Briant, 1995, "Combinatorial Chemistry Library Design using Pharmacophore Diversity," *Id.*, Pavia, 1996, "Chemically Generated Screening Libraries: Present and Future," *Id.*; and U.S. Patents, Nos. 5,880,972 to Horlbeck; 5,463,564 to Agrafiotis *et al.*; 5,331573 to Balaji *et al.*; and 5,573,905 to Lerner *et al.*

The invention also provides antibacterial and antiviral methods. The invention provides methods for blocking endoproteolytic activation of bacterial toxins. Bacterial targets of the antibacterial methods provided by this invention include but are not limited to any bacteria that produces an endoproteolytically-activated toxin, such as diphtheria toxin produced by *Corynebacterium diptheriae,* exotoxin A of *Pseudomonas aurigenosa,* tetanus toxin, the enterotoxins of *Escherichia coli* and *Vibrio cholerae,* protective antigen of *Bacillus anthracis* and the neurotoxin and C2 toxin of *Clostridium botulinum.* Preferred toxins are those that are proteolytically processed at a consensus furin recognition site (-Arg-Xaa-Xaa-Arg-). Preferred embodiments include *Corynebacterium diptheriae, Pseudomonas aeruginosa* and *Bacillis anthracis.*

Viral targets of antiviral methods provided include but are not limited to picornaviruses (*e.g.*, poliovirus and rhinovirus); orthomyxovirusus (*e.g.*, influenza virus); paramyxoviruses (*e.g.*, measles virus and mumps virus); coronaviruses; rhabdoviruses (*e.g.*, rabies virus and vesicular stomatitis virus); togaviruses (*e.g.*, Semliki Forest virus and yellow fever virus); bunyaviruses (*e.g.*, California encephalitis virus); arenaviruses (*e.g.*, Lassa fever virus); rubella virus; reoviruses (*e.g.*, Colorado tick fever virus); hepatitis viruses; adenoviruses; herpesviruses (*e.g.*, herpes simplex virus); and oncogenic viruses, including papilloma viruses, RNA tumor viruses, or retroviruses, and lentiviruses (*e.g.*, human immune deficiency virus). The most preferred viruses are the human immunodeficiency viruses (HIV-1 and HIV-2) and human cytomegalovirus (HCMV).

Cells intended to be protected by the methods provided by this invention include but are not limited to human, canine, bovine, murine, leporine, porcine, ovine, simian,

feline, hircine, and equine cells. The preferred cells are human cells. More preferred cells are human T lymphocytes (T cells), and the most preferred human T cells are those human T cells expressing the cell surface antigen CD4.

The methods of the present invention may be used to treat donated human blood or plasma to protect transfusion recipients from viral infection from contaminating virus. The methods of the present invention may be used to treat human semen to protect embryos derived from such semen, and mothers bearing such embryos or impregnated with such semen, from contaminating virus. In a preferred embodiment, the contaminating virus is HIV-1. In another preferred embodiment, the contaminating virus is HCMV.

The present invention provides methods for inhibiting bacterial infection in a human. The invention also provided for treating a human infected with a bacteria. These methods provided by the invention comprise the step of administering a therapeutically-effective amount of a peptide or peptide mimetic of the invention to the human, most preferably as a pharmaceutical composition comprising a pharmaceutically-acceptable carrier. The invention also provides pharmaceutically acceptable compositions effective for use with the methods provided by the invention comprising the peptides and peptide mimetics of the invention and a pharmaceutically acceptable carrier.

The present invention provides methods for inhibiting viral infection in a human. The invention also provided for treating a human infected with a virus. These methods provided by the invention comprise the step of administering a therapeutically-effective amount of a peptide or peptide mimetic of the invention to the human, most preferably as a pharmaceutical composition comprising a pharmaceutically-acceptable carrier. Preferred viruses of these embodiments of the invention are HIV-1 and HCMV. The invention also provides pharmaceutically acceptable compositions effective for use with the methods provided by the invention comprising the peptides and peptide mimetics of the invention and a pharmaceutically acceptable carrier.

Another embodiment of the present invention includes methods for treating immunosuppression in a human associated with viral infection. Yet another embodiment of the present invention provides a method of prophylaxis for treating a human exposed to infection with a virus, in a particular those directly at risk of infection as a result of intimate contact with humans infected with a virus of tissues or bodily

fluids contaminated by a virus. The preferred virus of these embodiments of the invention is HIV-1. The invention also provides pharmaceutically acceptable compositions effective for use with the methods provided by the invention comprising the peptides and peptide mimetics of the invention and a pharmaceutically acceptable carrier.

The invention also provides methods for inhibiting proteolytic processing of a biologically active protein or peptide in a cell comprising contacting such cells with the gene therapy delivery system of the invention. The methods of the invention encompass inhibition of proteolytic processing of any biologically active molecule that is proteolytically processed by furin *in vivo* or *in vitro*, including but not limited to peptide hormones, neuropeptides, growth factors, coagulation factors, serum albumin, cell surface receptors, and adhesion molecules. Preferred biologically active proteins are pro-β-nerve growth factor, blood coagulation factor protein Factor IX, pro-von Willibrand factor, complement factor C3 and renin, for alleviation of pathological conditions and disease states in an animal, preferably a human, associated with over-expression, over-production or otherwise inappropriate synthesis of such biologically-active proteins.

Preparation of pharmaceutically acceptable compositions provided by the present invention can be prepared using methods well know to those with skill in the art. Any of the common pharmaceutical-acceptable carriers such as sterile saline solution, plasma, etc., can be utilized for preparing the pharmaceutical compositions provided by the invention. Routes of administration include but are not limited to oral, nasal (including inhalation into the lungs), intravenous, parenteral, rectal, optical, aural and transdermal. The pharmaceutical compositions of the invention may be administered intravenously in any conventional medium for intravenous injection such as a aqueous saline medium, or in blood plasma medium. Such medium may also contain conventional pharmaceutical adjunct materials such as, for example, pharmaceutically acceptable salts to adjust the osmotic pressure, buffers, preservatives and the like. Among the preferred media are normal saline and plasma.

Formulations may further include one or more diluents, fillers, emulsifiers, preservatives, buffers, excipients, and the like, and may be provided in such forms as liquids, powders, emulsions, suppositories, liposomes, transdermal patches and tablets, for example. The agents of the present invention can be formulated according to known

methods to prepare pharmaceutically useful compositions, whereby these materials, or their functional derivatives, are combined in admixture with a pharmaceutically acceptable carrier vehicle. Suitable vehicles and their formulation, inclusive of other human proteins, *e.g.*, human serum albumin, are described, for example, in REMINGTON'S PHARMACEUTICAL SCIENCES (1980, 16th ed., Osol, ed., Mack Press:Easton PA).

Additional pharmaceutical methods may be employed to control the duration of action. Control release preparations may be achieved through the use of polymers to complex or absorb a mimetic of the invention. Such controlled delivery may be exercised by selecting appropriate macromolecules (for example polyesters, polyamino acids, polyvinyl pyrrolidone, ethylenevinylacetate, methylcellulose, carboxymethylcellulose, or protamine, sulfate) and the concentration of macromolecules as well as the methods of incorporation in order to control release. Another possible method to control the duration of action by controlled release preparations is to incorporate a peptide or peptide mimetic of the invention into particles of a polymeric material such as polyesters, polyamino acids, hydrogels, poly(lactic acid) or ethylene vinylacetate copolymers. Alternatively, instead of incorporating these agents into polymeric particles, it is possible to entrap these materials in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatine-microcapsules and poly(methylmethacylate) microcapsules, respectively, or in colloidal drug delivery systems, for example, liposomes, albumin microspheres, microemulsions, nanoparticles, and nanocapsules or in macroemulsions. Such techniques are disclosed in REMINGTON'S PHARMACEUTICAL SCIENCES (1980).

Compositions for parenteral administration include sterile aqueous or non-aqueous solutions, suspensions, and emulsions. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oils such as olive oil, and injectable organic esters such as ethyl oleate. Carriers, adjuncts or occlusive dressings can be used to increase tissue permeability and enhance antigen absorption. Liquid dosage forms for oral administration may generally comprise a liposome solution containing the liquid dosage form. Suitable forms for suspending liposomes include emulsions, suspensions, solutions, syrups, and elixirs containing inert diluents commonly used in the art, such as purified water. Besides the inert diluents, such compositions can also include wetting

agents, emulsifying and suspending agents, or sweetening, flavoring, coloring or perfuming agents.

A composition is said to be "pharmacologically acceptable" if its administration can be tolerated by a recipient patient. Such an agent is said to be administered in a "therapeutically effective amount" if the amount administered is physiologically significant. An agent is physiologically significant if its presence results in a detectable change in the physiology of a recipient patient.

Generally, the dosage needed to provide an effective amount of the composition will vary depending upon such factors as the recipient's age, condition, gender, and extent of disease, if any, and other variables which can be adjusted by one of ordinary skill in the art. The pharmaceutical compositions and medicaments of the invention are preferably in the form of a unit dose in solid, semi-solid and liquid dosage forms such as tablets, pills, powders, liquid solutions or suspensions, and injectable and infusible solutions. Effective dosage ranges from about 100 μg/kg to about 10 mg/kg of body weight are contemplated.

The Examples which follow are illustrative of specific embodiments of the invention, and various uses thereof. They set forth for explanatory purposes only, and are not to be taken as limiting the invention.

EXAMPLE 1

Furin Inhibition Assay

In order to assess the biological activity of the mimetics of the invention, a furin inhibition assay was developed as follows.

A model system was prepared for assaying furin-catalyzed maturation of *Pseudomonas aeruginosa* exotoxion A (PEA), as shown in Figures 2, 3 and 4. *P. aeruginosa* pro-exotoxion A is cleaved at the sequence Arg-Gln-Pro-Arg_{279} in the II + Ib subunit of the toxin in endosomes of infected cells (Figure 2). In the assay, illustrated in Figure 3, A7 cells were incubated in the presence and absence of test PDX mimetics of the invention for 1h under cell culture conditions. The media containing the mimetic was then exchanged for fresh media containing a growth-inhibitory amount of pro-PEA, and incubated under cell culture conditions for 6h. Thereafter, the cells were metabolically labeled with ^{35}S-labeled methionine and/or cysteine for 30min, and

cellular proteins precipitated with trichloroacetic acid. PDX itself or an Arg-Xaa-Xaa-Arg-containing peptide was used as a positive control, and α_1-antitrypsin Pittsburgh (PIT; SEQ ID No. 6) was used as a negative control in these assays.

The results of a standardized test assay showing the difference in protein synthesis in the presence of PDX or PIT is shown in Figure 4. Preincubation of A7 cells in the presence of increasing concentrations of PDX resulted in increasing levels of protein synthesis in the presence of PEA compared with cells incubated without PDX. In contrast, little or no protective effect was observed by incubating A7 cells with PIT at any concentration tested. These results indicated that the assay was effective in detecting PDX-mediated inhibition of furin-catalyzed maturation of pro-PEA.

An alternative assay was used to demonstrate inhibition of furin-mediated maturation of human cytomegalovirus (HCMV) glycoprotein gB. This assay is illustrated in Figures 2, and 5 through 8. HCMV glycoprotein pro-gB is cleaved at the sequence Arg-Thr-Lys-Arg_{465} in the pro-protein, yielding gp110 and gp55, linked by a disulfide bond, as shown in Figure 5. In the assay, illustrated in Figure 6, U373 cells were infected with HCMV Towne at a multiplicity of infection of about 0.1. After infection, the putative inhibitor was added and incubated with the infected cells for 5 days under cell culture conditions. Cell extracts were then prepared and used to infect a naive culture of human foreskin fibroblasts (HFF), which were incubated in the absence of inhibitor for 7 days. These cells were immobilized under agar using conventional techniques, and the number of infected viral plaques determined by counting. Foscarnet, a phosphate group analog and known HCMV inhibitor, was assayed in parallel as a positive control.

The results of a standardized test assay using PDX and foscarnet are shown in Figure 7. PDX has an ED_{50} that is about ten-fold lower than foscarnet for plaque formation, illustrating its enhanced inhibitory capacity. These results indicated that the assay was effective in detecting PDX-mediated inhibition of furin-catalyzed maturation of HCMV glycoprotein gB.

In an additional or alternative embodiment of this assay, parallel cultures of infected U373 cells were grown in the presence of inhibitor and cellular proteins isolated after 5 days of infected cell growth. Sodium dodecyl sulfate/polyacrylamide gel electrophoresis (SDS/PAGE) was performed on the cellular protein extract, followed by Western blotting and hybridization with an immunological reagent specific for

glycoprotein gB, all techniques performed as described in Sambrook *et al.* (1989, MOLECULAR CLONING: A LABORATORY MANUAL, CSPLP: New York). In these assays PDX itself or an Arg-Xaa-Xaa-Arg-containing peptide was used as a positive control, and α_1-antitrypsin Pittsburgh (PIT; SEQ ID No. 6) was used as a negative control.

The results of a standardized test assay showing the difference in HCMV glycoprotein gB maturation in the presence of PDX or PIT is shown in Figure 8. In the absence of either PDX or PIT, infected cells were observed to contain predominantly gp110 and gp55, separated by treatment with β-mercaptoethanol prior to SDS-PAGE analysis (lane labeled gB/Wt in the Figure). A similar level of cleavage was seen for cells incubated with the PIT variant of α_1-antitrypsin (lane labeled gB/PIT) In contrast, the predominant band observed in the cell extract from infected cells incubated in the presence of PDX was pro-gB (lane labeled gB/PDX). These results indicated that the assay was effective in detecting PDX-mediated inhibition of furin-catalyzed maturation of HCMV glycoprotein gB.

These assays are used to characterize the furin inhibitory capacity of the mimetic compounds of the invention. Preferably, cells are incubated in varying concentrations of the mimetic, in parallel with a standardized concentration of PDX or an Arg-Xaa-Xaa-Arg-containing peptide. Furin inhibitory capacity of putatuve mimetics of the invention are characterized by quantitative comparisons of the extent of furin inhibition, measured as described herein by ED_{50} of plaque formation, percent protein synthesis, or K_i of furin activity, to PDX or Arg-Xaa-Xaa-Arg-containing peptides of the invention.

It should be understood that the foregoing disclosure emphasizes certain specific embodiments of the invention and that all modifications or alternatives equivalent thereto are within the spirit and scope of the invention as set forth in the appended claims. The disclosure of all patents, patent applications and publications are hereby incorporated by reference herein in their entirety.

APPENDIX A

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HEADER:     PROTEIN                                    18-MAR-98
COMPND:     Alphal-PDX:
AUTHOR:     Francois Jean: GENERATED BY SYBYL, A PRODUCT OF TRIPOS
ASSOCIATES, INC.
SEQRES    1    372  PHE ASN LYS ILE THR PRO ASN LEU ALA GLU PHE ALA PHE
SEQRES    2    372  SER LEU TYR ARG GLN LEU ALA HIS GLN SER ASN SER THR
SEQRES    3    372  ASN ILE LEU PHE SER PRO VAL SER ILE ALA THR ALA PHE
SEQRES    4    372  ALA MET LEU SER LEU GLY THR LYS ALA ASP THR HIS ASP
SEQRES    5    372  GLU ILE LEU GLU GLY LEU ASN PHE ASN LEU THR GLU ILE
SEQRES    6    372  PRO GLU ALA GLN ILE HIS GLU GLY PHE GLN GLU LEU LEU
SEQRES    7    372  ARG THR LEU ASN GLN PRO ASP SER GLN LEU GLN LEU THR
SEQRES    8    372  THR GLY ASN GLY LEU PHE LEU SER GLU GLY LEU LYS LEU
SEQRES    9    372  VAL ASP LYS PHE LEU GLU ASP VAL LYS LYS LEU TYR HIS
SEQRES   10    372  SER GLU ALA PHE THR VAL ASN PHE GLY ASP THR GLU GLU
SEQRES   11    372  ALA LYS LYS GLN ILE ASN ASP TYR VAL GLU LYS GLY THR
SEQRES   12    372  GLN GLY LYS ILE VAL ASP LEU VAL LYS GLU LEU ASP ARG
SEQRES   13    372  ASP THR VAL PHE ALA LEU VAL ASN TYR ILE PHE PHE LYS
SEQRES   14    372  GLY LYS TRP GLU ARG PRO PHE GLU VAL LYS ASP THR GLU
SEQRES   15    372  GLU GLU ASP PHE HIS VAL ASP GLN VAL THR THR VAL LYS
SEQRES   16    372  VAL PRO MET MET LYS ARG LEU GLY MET PHE ASN ILE GLN
SEQRES   17    372  HIS CYS LYS LYS LEU SER SER TRP VAL LEU LEU MET LYS
SEQRES   18    372  TYR LEU GLY ASN ALA THR ALA ILE PHE PHE LEU PRO ASP
SEQRES   19    372  GLU GLY LYS LEU GLN HIS LEU GLU ASN GLU LEU THR HIS
SEQRES   20    372  ASP ILE ILE THR LYS PHE LEU GLU ASN GLU ASP ARG ARG
SEQRES   21    372  SER ALA SER LEU HIS LEU PRO LYS LEU SER ILE THR GLY
SEQRES   22    372  THR TYR ASP LEU LYS SER VAL LEU GLY GLN LEU GLY ILE
SEQRES   23    372  THR LYS VAL PHE SER ASN GLY ALA ASP LEU SER GLY VAL
SEQRES   24    372  THR GLU GLU ALA PRO LEU LYS LEU SER LYS ALA VAL HIS
SEQRES   25    372  LYS ALA VAL LEU THR ILE ASP GLU LYS GLY THR GLU ALA
SEQRES   26    372  ALA GLY ALA MET PHE LEU GLU ARG ILE PRO ARG SER ILE
SEQRES   27    372  PRO PRO GLU VAL LYS PHE ASN LYS PRO PHE VAL PHE LEU
SEQRES   28    372  MET ILE GLU GLN ASN THR LYS SER PRO LEU PHE MET GLY
SEQRES   29    372  LYS VAL VAL ASN PRO THR GLN LYS
ATOM      1  N    PHE   23      -5.833  16.226  -6.690  1.00 23.61
ATOM      2  CA   PHE   23      -5.581  16.146  -8.162  1.00 22.30
ATOM      3  C    PHE   23      -4.949  14.813  -8.503  1.00 27.28
ATOM      4  O    PHE   23      -4.316  14.204  -7.657  1.00 30.22
ATOM      5  CB   PHE   23      -4.683  17.297  -8.647  1.00 23.48
ATOM      6  CG   PHE   23      -3.343  17.340  -7.974  1.00 24.85
ATOM      7  CD1  PHE   23      -3.166  18.068  -6.790  1.00 27.54
ATOM      8  CD2  PHE   23      -2.252  16.649  -8.512  1.00 28.27
ATOM      9  CE1  PHE   23      -1.910  18.106  -6.144  1.00 31.11
ATOM     10  CE2  PHE   23      -0.991  16.676  -7.881  1.00 29.35
ATOM     11  CZ   PHE   23      -0.819  17.409  -6.694  1.00 29.09
ATOM     12  N    ASN   24      -5.012  14.457  -9.781  1.00 21.95
ATOM     13  CA   ASN   24      -4.526  13.181 -10.299  1.00 22.18
ATOM     14  C    ASN   24      -3.772  13.430 -11.610  1.00 27.00
ATOM     15  O    ASN   24      -4.015  14.434 -12.289  1.00 27.82
ATOM     16  CB   ASN   24      -5.739  12.281 -10.583  1.00 22.61
ATOM     17  CG   ASN   24      -6.844  12.467  -9.568  1.00 53.45
ATOM     18  OD1  ASN   24      -6.682  12.147  -8.396  1.00 51.94
ATOM     19  ND2  ASN   24      -7.938  13.068  -9.996  1.00 50.72
ATOM     20  N    LYS   25      -2.888  12.509 -11.981  1.00 23.21
ATOM     21  CA   LYS   25      -2.112  12.664 -13.216  1.00 23.36
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ATOM	22	C	LYS	25	-1.863	11.278	-13.835	1.00	30.07
ATOM	23	O	LYS	25	-2.147	11.045	-15.016	1.00	32.07
ATOM	24	CB	LYS	25	-0.780	13.350	-12.867	1.00	25.58
ATOM	25	CG	LYS	25	-0.046	14.055	-14.012	1.00	44.07
ATOM	26	CD	LYS	25	1.032	14.953	-13.430	1.00	53.95
ATOM	27	CE	LYS	25	2.011	15.488	-14.465	1.00	71.25
ATOM	28	NZ	LYS	25	3.041	16.381	-13.843	1.00	88.52
ATOM	29	N	ILE	26	-1.364	10.360	-13.003	1.00	23.41
ATOM	30	CA	ILE	26	-1.080	8.977	-13.397	1.00	19.71
ATOM	31	C	ILE	26	-1.881	8.077	-12.454	1.00	22.13
ATOM	32	O	ILE	26	-1.928	6.862	-12.636	1.00	20.14
ATOM	33	CB	ILE	26	0.431	8.626	-13.237	1.00	20.71
ATOM	34	CG1	ILE	26	0.800	8.525	-11.759	1.00	18.42
ATOM	35	CG2	ILE	26	1.292	9.669	-13.907	1.00	22.50
ATOM	36	CD1	ILE	26	2.225	8.160	-11.516	1.00	7.76
ATOM	37	N	THR	27	-2.535	8.697	-11.470	1.00	18.07
ATOM	38	CA	THR	27	-3.312	7.978	-10.472	1.00	18.05
ATOM	39	C	THR	27	-4.328	7.029	-11.048	1.00	21.15
ATOM	40	O	THR	27	-4.554	5.960	-10.482	1.00	22.20
ATOM	41	CB	THR	27	-4.013	8.924	-9.507	1.00	30.10
ATOM	42	OG1	THR	27	-5.184	9.463	-10.134	1.00	38.18
ATOM	43	CG2	THR	27	-3.080	10.036	-9.116	1.00	31.04
ATOM	44	N	PRO	28	-4.995	7.414	-12.147	1.00	16.92
ATOM	45	CA	PRO	28	-5.951	6.424	-12.631	1.00	16.23
ATOM	46	C	PRO	28	-5.213	5.159	-13.050	1.00	21.85
ATOM	47	O	PRO	28	-5.700	4.044	-12.837	1.00	21.37
ATOM	48	CB	PRO	28	-6.672	7.139	-13.782	1.00	17.43
ATOM	49	CG	PRO	28	-5.805	8.336	-14.120	1.00	23.33
ATOM	50	CD	PRO	28	-5.158	8.716	-12.819	1.00	18.87
ATOM	51	N	ASN	29	-3.978	5.350	-13.515	1.00	19.08
ATOM	52	CA	ASN	29	-3.127	4.249	-13.957	1.00	18.64
ATOM	53	C	ASN	29	-2.694	3.448	-12.733	1.00	21.94
ATOM	54	O	ASN	29	-2.648	2.223	-12.768	1.00	23.88
ATOM	55	CB	ASN	29	-1.899	4.770	-14.725	1.00	19.53
ATOM	56	CG	ASN	29	-2.261	5.486	-16.027	1.00	48.12
ATOM	57	OD1	ASN	29	-2.498	4.852	-17.054	1.00	41.88
ATOM	58	ND2	ASN	29	-2.252	6.819	-15.999	1.00	43.32
ATOM	59	N	LEU	30	-2.441	4.136	-11.627	1.00	16.53
ATOM	60	CA	LEU	30	-2.033	3.466	-10.392	1.00	16.25
ATOM	61	C	LEU	30	-3.195	2.744	-9.735	1.00	22.44
ATOM	62	O	LEU	30	-3.013	1.679	-9.147	1.00	23.44
ATOM	63	CB	LEU	30	-1.405	4.464	-9.402	1.00	16.22
ATOM	64	CG	LEU	30	-0.017	5.008	-9.772	1.00	20.92
ATOM	65	CD1	LEU	30	0.443	6.007	-8.746	1.00	20.56
ATOM	66	CD2	LEU	30	0.989	3.875	-9.911	1.00	22.13
ATOM	67	N	ALA	31	-4.390	3.311	-9.873	1.00	19.06
ATOM	68	CA	ALA	31	-5.618	2.752	-9.301	1.00	17.69
ATOM	69	C	ALA	31	-5.914	1.378	-9.880	1.00	20.90
ATOM	70	O	ALA	31	-6.024	0.387	-9.152	1.00	18.85
ATOM	71	CB	ALA	31	-6.790	3.681	-9.570	1.00	18.32
ATOM	72	N	GLU	32	-6.041	1.328	-11.198	1.00	19.72
ATOM	73	CA	GLU	32	-6.316	0.081	-11.879	1.00	20.59
ATOM	74	C	GLU	32	-5.190	-0.921	-11.671	1.00	24.22
ATOM	75	O	GLU	32	-5.393	-2.135	-11.765	1.00	25.34

ATOM	76	CB	GLU	32	-6.610	0.341	-13.358	1.00	22.34
ATOM	77	CG	GLU	32	-7.765	1.321	-13.585	1.00	31.78
ATOM	78	CD	GLU	32	-9.057	0.949	-12.858	1.00	49.18
ATOM	79	OE1	GLU	32	-9.177	-0.176	-12.328	1.00	28.81
ATOM	80	OE2	GLU	32	-9.977	1.790	-12.837	1.00	50.57
ATOM	81	N	PHE	33	-4.011	-0.404	-11.354	1.00	18.26
ATOM	82	CA	PHE	33	-2.856	-1.244	-11.050	1.00	16.77
ATOM	83	C	PHE	33	-3.087	-1.883	-9.669	1.00	18.47
ATOM	84	O	PHE	33	-2.928	-3.091	-9.486	1.00	14.96
ATOM	85	CB	PHE	33	-1.573	-0.406	-11.061	1.00	17.37
ATOM	86	CG	PHE	33	-0.397	-1.090	-10.439	1.00	17.39
ATOM	87	CD1	PHE	33	0.130	-2.245	-10.998	1.00	21.30
ATOM	88	CD2	PHE	33	0.161	-0.597	-9.269	1.00	19.00
ATOM	89	CE1	PHE	33	1.203	-2.903	-10.397	1.00	22.86
ATOM	90	CE2	PHE	33	1.228	-1.242	-8.660	1.00	21.58
ATOM	91	CZ	PHE	33	1.751	-2.399	-9.222	1.00	20.43
ATOM	92	N	ALA	34	-3.567	-1.066	-8.740	1.00	16.77
ATOM	93	CA	ALA	34	-3.863	-1.492	-7.379	1.00	15.77
ATOM	94	C	ALA	34	-4.936	-2.562	-7.385	1.00	21.38
ATOM	95	O	ALA	34	-4.844	-3.548	-6.666	1.00	23.09
ATOM	96	CB	ALA	34	-4.319	-0.311	-6.557	1.00	15.65
ATOM	97	N	PHE	35	-5.947	-2.381	-8.221	1.00	17.88
ATOM	98	CA	PHE	35	-7.033	-3.350	-8.305	1.00	16.95
ATOM	99	C	PHE	35	-6.574	-4.663	-8.917	1.00	20.50
ATOM	100	O	PHE	35	-6.896	-5.740	-8.426	1.00	20.02
ATOM	101	CB	PHE	35	-8.195	-2.771	-9.106	1.00	18.28
ATOM	102	CG	PHE	35	-8.825	-1.551	-8.479	1.00	19.41
ATOM	103	CD1	PHE	35	-8.854	-1.392	-7.097	1.00	22.41
ATOM	104	CD2	PHE	35	-9.389	-0.561	-9.269	1.00	21.84
ATOM	105	CE1	PHE	35	-9.437	-0.264	-6.522	1.00	25.39
ATOM	106	CE2	PHE	35	-9.974	0.568	-8.697	1.00	22.84
ATOM	107	CZ	PHE	35	-9.998	0.715	-7.329	1.00	22.70
ATOM	108	N	SER	36	-5.763	-4.558	-9.959	1.00	18.62
ATOM	109	CA	SER	36	-5.232	-5.714	-10.659	1.00	18.48
ATOM	110	C	SER	36	-4.386	-6.509	-9.685	1.00	19.66
ATOM	111	O	SER	36	-4.593	-7.701	-9.491	1.00	19.74
ATOM	112	CB	SER	36	-4.387	-5.258	-11.853	1.00	20.88
ATOM	113	OG	SER	36	-4.134	-6.331	-12.735	1.00	27.56
ATOM	114	N	LEU	37	-3.499	-5.811	-8.998	1.00	14.84
ATOM	115	CA	LEU	37	-2.626	-6.459	-8.037	1.00	15.38
ATOM	116	C	LEU	37	-3.417	-7.009	-6.844	1.00	20.75
ATOM	117	O	LEU	37	-3.014	-7.991	-6.228	1.00	21.25
ATOM	118	CB	LEU	37	-1.536	-5.483	-7.586	1.00	15.68
ATOM	119	CG	LEU	37	-0.433	-5.990	-6.656	1.00	22.62
ATOM	120	CD1	LEU	37	0.354	-7.114	-7.294	1.00	23.86
ATOM	121	CD2	LEU	37	0.480	-4.836	-6.336	1.00	26.39
ATOM	122	N	TYR	38	-4.602	-6.454	-6.613	1.00	17.53
ATOM	123	CA	TYR	38	-5.457	-6.869	-5.510	1.00	17.17
ATOM	124	C	TYR	38	-6.204	-8.160	-5.836	1.00	21.99
ATOM	125	O	TYR	38	-6.054	-9.175	-5.148	1.00	22.31
ATOM	126	CB	TYR	38	-6.443	-5.751	-5.153	1.00	16.94
ATOM	127	CG	TYR	38	-7.398	-6.137	-4.054	1.00	17.29
ATOM	128	CD1	TYR	38	-7.050	-5.991	-2.715	1.00	17.57
ATOM	129	CD2	TYR	38	-8.616	-6.744	-4.352	1.00	19.23

ATOM	130	CE1	TYR	38	-7.890	-6.453	-1.704	1.00	17.18
ATOM	131	CE2	TYR	38	-9.453	-7.203	-3.350	1.00	20.11
ATOM	132	CZ	TYR	38	-9.085	-7.058	-2.037	1.00	24.15
ATOM	133	OH	TYR	38	-9.915	-7.535	-1.063	1.00	26.53
ATOM	134	N	ARG	39	-6.979	-8.121	-6.913	1.00	17.51
ATOM	135	CA	ARG	39	-7.761	-9.263	-7.383	1.00	17.33
ATOM	136	C	ARG	39	-6.856	-10.469	-7.617	1.00	19.96
ATOM	137	O	ARG	39	-7.296	-11.617	-7.538	1.00	19.48
ATOM	138	CB	ARG	39	-8.526	-8.870	-8.656	1.00	17.17
ATOM	139	CG	ARG	39	-9.451	-7.667	-8.419	1.00	24.64
ATOM	140	CD	ARG	39	-10.224	-7.239	-9.648	1.00	34.67
ATOM	141	NE	ARG	39	-11.117	-6.112	-9.378	1.00	44.73
ATOM	142	CZ	ARG	39	-10.927	-4.885	-9.849	1.00	66.12
ATOM	143	NH1	ARG	39	-9.879	-4.622	-10.616	1.00	58.52
ATOM	144	NH2	ARG	39	-11.786	-3.920	-9.552	1.00	57.78
ATOM	145	N	GLN	40	-5.581	-10.172	-7.833	1.00	16.43
ATOM	146	CA	GLN	40	-4.525	-11.145	-8.058	1.00	17.01
ATOM	147	C	GLN	40	-4.296	-11.946	-6.780	1.00	24.64
ATOM	148	O	GLN	40	-4.377	-13.176	-6.757	1.00	26.03
ATOM	149	CB	GLN	40	-3.242	-10.379	-8.399	1.00	18.53
ATOM	150	CG	GLN	40	-2.028	-11.234	-8.646	1.00	32.27
ATOM	151	CD	GLN	40	-2.196	-12.108	-9.853	1.00	65.70
ATOM	152	OE1	GLN	40	-2.982	-11.814	-10.756	1.00	68.30
ATOM	153	NE2	GLN	40	-1.469	-13.194	-9.876	1.00	60.66
ATOM	154	N	LEU	41	-4.036	-11.213	-5.711	1.00	20.30
ATOM	155	CA	LEU	41	-3.769	-11.784	-4.412	1.00	19.36
ATOM	156	C	LEU	41	-5.054	-12.277	-3.745	1.00	25.88
ATOM	157	O	LEU	41	-5.039	-13.298	-3.048	1.00	26.53
ATOM	158	CB	LEU	41	-3.067	-10.724	-3.540	1.00	18.71
ATOM	159	CG	LEU	41	-1.757	-10.130	-4.089	1.00	23.44
ATOM	160	CD1	LEU	41	-1.403	-8.856	-3.362	1.00	22.82
ATOM	161	CD2	LEU	41	-0.631	-11.142	-3.986	1.00	26.55
ATOM	162	N	ALA	42	-6.175	-11.626	-4.053	1.00	21.70
ATOM	163	CA	ALA	42	-7.468	-11.968	-3.442	1.00	20.36
ATOM	164	C	ALA	42	-8.019	-13.311	-3.903	1.00	25.53
ATOM	165	O	ALA	42	-8.771	-13.955	-3.176	1.00	26.06
ATOM	166	CB	ALA	42	-8.502	-10.856	-3.683	1.00	20.25
ATOM	167	N	HIS	43	-7.688	-13.705	-5.130	1.00	20.57
ATOM	168	CA	HIS	43	-8.147	-14.981	-5.657	1.00	20.04
ATOM	169	C	HIS	43	-7.203	-16.082	-5.208	1.00	24.10
ATOM	170	O	HIS	43	-7.619	-17.009	-4.509	1.00	23.78
ATOM	171	CB	HIS	43	-8.237	-14.960	-7.186	1.00	21.07
ATOM	172	CG	HIS	43	-9.585	-14.594	-7.708	1.00	25.01
ATOM	173	ND1	HIS	43	-9.950	-13.285	-7.989	1.00	27.71
ATOM	174	CD2	HIS	43	-10.683	-15.348	-7.974	1.00	26.92
ATOM	175	CE1	HIS	43	-11.203	-13.258	-8.411	1.00	27.25
ATOM	176	NE2	HIS	43	-11.661	-14.495	-8.418	1.00	27.36
ATOM	177	N	GLN	44	-5.941	-15.956	-5.615	1.00	20.85
ATOM	178	CA	GLN	44	-4.877	-16.901	-5.276	1.00	21.40
ATOM	179	C	GLN	44	-4.960	-17.227	-3.797	1.00	27.47
ATOM	180	O	GLN	44	-5.420	-18.303	-3.403	1.00	27.52
ATOM	181	CB	GLN	44	-3.518	-16.267	-5.590	1.00	23.51
ATOM	182	CG	GLN	44	-2.319	-16.941	-4.935	1.00	67.92
ATOM	183	CD	GLN	44	-1.087	-16.070	-4.998	1.00	109.81

ATOM	184	OE1	GLN	44	-1.078	-15.031	-5.662	1.00109.42
ATOM	185	NE2	GLN	44	-0.045	-16.469	-4.288	1.00109.97
ATOM	186	N	SER	45	-4.545	-16.255	-2.995	1.00 26.78
ATOM	187	CA	SER	45	-4.570	-16.361	-1.544	1.00 27.70
ATOM	188	C	SER	45	-6.057	-16.282	-1.198	1.00 33.50
ATOM	189	O	SER	45	-6.787	-15.491	-1.800	1.00 37.36
ATOM	190	CB	SER	45	-3.789	-15.194	-0.941	1.00 31.49
ATOM	191	OG	SER	45	-3.343	-15.506	0.359	1.00 47.22
ATOM	192	N	ASN	46	-6.507	-17.107	-0.260	1.00 27.55
ATOM	193	CA	ASN	46	-7.930	-17.130	0.093	1.00 27.41
ATOM	194	C	ASN	46	-8.360	-16.608	1.471	1.00 28.59
ATOM	195	O	ASN	46	-9.262	-15.772	1.567	1.00 29.04
ATOM	196	CB	ASN	46	-8.533	-18.519	-0.183	1.00 33.22
ATOM	197	CG	ASN	46	-7.501	-19.636	-0.130	1.00 74.24
ATOM	198	OD1	ASN	46	-6.480	-19.544	0.577	1.00 66.23
ATOM	199	ND2	ASN	46	-7.767	-20.708	-0.870	1.00 69.34
ATOM	200	N	SER	47	-7.744	-17.107	2.538	1.00 23.10
ATOM	201	CA	SER	47	-8.091	-16.653	3.888	1.00 22.42
ATOM	202	C	SER	47	-6.920	-15.935	4.568	1.00 27.21
ATOM	203	O	SER	47	-6.515	-16.296	5.673	1.00 27.54
ATOM	204	CB	SER	47	-8.578	-17.824	4.742	1.00 24.67
ATOM	205	OG	SER	47	-9.992	-17.784	4.892	1.00 37.40
ATOM	206	N	THR	48	-6.414	-14.889	3.912	1.00 24.53
ATOM	207	CA	THR	48	-5.269	-14.126	4.410	1.00 24.98
ATOM	208	C	THR	48	-5.488	-12.602	4.367	1.00 29.19
ATOM	209	O	THR	48	-6.179	-12.102	3.477	1.00 32.29
ATOM	210	CB	THR	48	-4.005	-14.482	3.564	1.00 37.64
ATOM	211	OG1	THR	48	-3.640	-15.851	3.794	1.00 44.67
ATOM	212	CG2	THR	48	-2.824	-13.591	3.903	1.00 37.25
ATOM	213	N	ASN	49	-4.942	-11.874	5.342	1.00 21.11
ATOM	214	CA	ASN	49	-5.067	-10.413	5.342	1.00 20.02
ATOM	215	C	ASN	49	-4.150	-10.014	4.197	1.00 25.63
ATOM	216	O	ASN	49	-3.078	-10.599	4.023	1.00 28.91
ATOM	217	CB	ASN	49	-4.565	-9.775	6.645	1.00 23.44
ATOM	218	CG	ASN	49	-5.366	-10.201	7.851	1.00 57.54
ATOM	219	OD1	ASN	49	-6.599	-10.128	7.845	1.00 44.13
ATOM	220	ND2	ASN	49	-4.679	-10.672	8.888	1.00 54.42
ATOM	221	N	ILE	50	-4.588	-9.067	3.383	1.00 19.43
ATOM	222	CA	ILE	50	-3.795	-8.628	2.247	1.00 17.16
ATOM	223	C	ILE	50	-3.352	-7.206	2.512	1.00 19.43
ATOM	224	O	ILE	50	-4.120	-6.415	3.043	1.00 20.29
ATOM	225	CB	ILE	50	-4.630	-8.692	0.942	1.00 19.64
ATOM	226	CG1	ILE	50	-5.152	-10.119	0.736	1.00 19.17
ATOM	227	CG2	ILE	50	-3.804	-8.221	-0.252	1.00 19.61
ATOM	228	CD1	ILE	50	-6.136	-10.249	-0.374	1.00 11.82
ATOM	229	N	LEU	51	-2.105	-6.885	2.194	1.00 15.23
ATOM	230	CA	LEU	51	-1.631	-5.526	2.401	1.00 15.02
ATOM	231	C	LEU	51	-0.471	-5.202	1.491	1.00 20.37
ATOM	232	O	LEU	51	0.576	-5.833	1.575	1.00 21.91
ATOM	233	CB	LEU	51	-1.217	-5.303	3.856	1.00 15.01
ATOM	234	CG	LEU	51	-0.860	-3.870	4.258	1.00 19.98
ATOM	235	CD1	LEU	51	-2.033	-2.949	4.017	1.00 19.60
ATOM	236	CD2	LEU	51	-0.437	-3.830	5.701	1.00 20.30
ATOM	237	N	PHE	52	-0.666	-4.247	0.594	1.00 15.96

ATOM	238	CA	PHE	52	0.399	-3.844	-0.303	1.00	15.36
ATOM	239	C	PHE	52	0.270	-2.368	-0.613	1.00	19.59
ATOM	240	O	PHE	52	-0.803	-1.788	-0.458	1.00	19.47
ATOM	241	CB	PHE	52	0.390	-4.676	-1.595	1.00	16.46
ATOM	242	CG	PHE	52	-0.890	-4.566	-2.394	1.00	16.66
ATOM	243	CD1	PHE	52	-1.957	-5.430	-2.155	1.00	17.01
ATOM	244	CD2	PHE	52	-1.014	-3.624	-3.410	1.00	16.97
ATOM	245	CE1	PHE	52	-3.108	-5.356	-2.912	1.00	18.40
ATOM	246	CE2	PHE	52	-2.165	-3.552	-4.166	1.00	16.88
ATOM	247	CZ	PHE	52	-3.210	-4.419	-3.917	1.00	15.91
ATOM	248	N	SER	53	1.383	-1.761	-1.006	1.00	14.83
ATOM	249	CA	SER	53	1.391	-0.357	-1.365	1.00	14.34
ATOM	250	C	SER	53	1.428	-0.278	-2.891	1.00	21.85
ATOM	251	O	SER	53	2.412	-0.704	-3.515	1.00	22.16
ATOM	252	CB	SER	53	2.609	0.332	-0.738	1.00	13.76
ATOM	253	OG	SER	53	2.700	1.710	-1.076	1.00	14.03
ATOM	254	N	PRO	54	0.317	0.151	-3.519	1.00	19.23
ATOM	255	CA	PRO	54	0.307	0.249	-4.977	1.00	17.87
ATOM	256	C	PRO	54	1.308	1.295	-5.408	1.00	21.51
ATOM	257	O	PRO	54	1.957	1.153	-6.443	1.00	22.63
ATOM	258	CB	PRO	54	-1.129	0.670	-5.276	1.00	18.91
ATOM	259	CG	PRO	54	-1.889	-0.022	-4.200	1.00	23.13
ATOM	260	CD	PRO	54	-1.052	0.321	-2.994	1.00	19.69
ATOM	261	N	VAL	55	1.539	2.243	-4.501	1.00	17.72
ATOM	262	CA	VAL	55	2.461	3.348	-4.717	1.00	17.45
ATOM	263	C	VAL	55	3.930	2.952	-4.583	1.00	23.27
ATOM	264	O	VAL	55	4.702	3.173	-5.511	1.00	22.83
ATOM	265	CB	VAL	55	2.158	4.528	-3.769	1.00	20.90
ATOM	266	CG1	VAL	55	3.299	5.529	-3.784	1.00	21.20
ATOM	267	CG2	VAL	55	0.882	5.220	-4.199	1.00	20.16
ATOM	268	N	SER	56	4.316	2.362	-3.450	1.00	21.09
ATOM	269	CA	SER	56	5.708	1.971	-3.240	1.00	21.01
ATOM	270	C	SER	56	6.175	1.003	-4.318	1.00	22.56
ATOM	271	O	SER	56	7.256	1.172	-4.891	1.00	22.87
ATOM	272	CB	SER	56	5.942	1.402	-1.822	1.00	23.93
ATOM	273	OG	SER	56	5.405	0.099	-1.647	1.00	27.29
ATOM	274	N	ILE	57	5.312	0.054	-4.664	1.00	15.52
ATOM	275	CA	ILE	57	5.654	-0.936	-5.680	1.00	14.94
ATOM	276	C	ILE	57	5.902	-0.298	-7.053	1.00	17.44
ATOM	277	O	ILE	57	6.986	-0.425	-7.615	1.00	16.01
ATOM	278	CB	ILE	57	4.562	-2.017	-5.806	1.00	18.06
ATOM	279	CG1	ILE	57	4.511	-2.876	-4.556	1.00	17.03
ATOM	280	CG2	ILE	57	4.844	-2.929	-6.974	1.00	20.11
ATOM	281	CD1	ILE	57	3.466	-3.942	-4.631	1.00	17.46
ATOM	282	N	ALA	58	4.894	0.394	-7.570	1.00	14.71
ATOM	283	CA	ALA	58	4.959	1.047	-8.866	1.00	15.31
ATOM	284	C	ALA	58	6.147	1.987	-8.999	1.00	22.96
ATOM	285	O	ALA	58	6.987	1.814	-9.885	1.00	25.76
ATOM	286	CB	ALA	58	3.670	1.790	-9.134	1.00	15.90
ATOM	287	N	THR	59	6.203	2.990	-8.131	1.00	16.71
ATOM	288	CA	THR	59	7.287	3.959	-8.132	1.00	14.91
ATOM	289	C	THR	59	8.656	3.253	-8.180	1.00	19.37
ATOM	290	O	THR	59	9.585	3.726	-8.835	1.00	17.29
ATOM	291	CB	THR	59	7.168	4.863	-6.887	1.00	11.03

ATOM	292	OG1	THR	59	5.843	5.400	-6.830	1.00	7.10
ATOM	293	CG2	THR	59	8.155	6.014	-6.946	1.00	4.73
ATOM	294	N	ALA	60	8.711	2.055	-7.604	1.00	17.18
ATOM	295	CA	ALA	60	9.922	1.246	-7.555	1.00	16.17
ATOM	296	C	ALA	60	10.247	0.670	-8.924	1.00	17.24
ATOM	297	O	ALA	60	11.380	0.744	-9.384	1.00	17.12
ATOM	298	CB	ALA	60	9.762	0.122	-6.551	1.00	16.99
ATOM	299	N	PHE	61	9.244	0.097	-9.571	1.00	13.66
ATOM	300	CA	PHE	61	9.423	-0.497	-10.888	1.00	14.45
ATOM	301	C	PHE	61	9.413	0.524	-12.019	1.00	24.16
ATOM	302	O	PHE	61	9.881	0.250	-13.122	1.00	25.72
ATOM	303	CB	PHE	61	8.412	-1.617	-11.119	1.00	15.76
ATOM	304	CG	PHE	61	8.907	-2.959	-10.671	1.00	17.86
ATOM	305	CD1	PHE	61	8.887	-3.314	-9.320	1.00	19.64
ATOM	306	CD2	PHE	61	9.440	-3.854	-11.594	1.00	21.88
ATOM	307	CE1	PHE	61	9.396	-4.536	-8.905	1.00	22.58
ATOM	308	CE2	PHE	61	9.952	-5.080	-11.186	1.00	22.88
ATOM	309	CZ	PHE	61	9.929	-5.421	-9.842	1.00	21.09
ATOM	310	N	ALA	62	8.984	1.738	-11.699	1.00	20.90
ATOM	311	CA	ALA	62	8.961	2.830	-12.661	1.00	19.14
ATOM	312	C	ALA	62	10.359	3.437	-12.637	1.00	24.17
ATOM	313	O	ALA	62	10.842	3.949	-13.636	1.00	26.12
ATOM	314	CB	ALA	62	7.936	3.865	-12.255	1.00	19.28
ATOM	315	N	MET	63	10.987	3.380	-11.472	1.00	18.82
ATOM	316	CA	MET	63	12.334	3.883	-11.258	1.00	17.35
ATOM	317	C	MET	63	13.304	2.892	-11.889	1.00	23.98
ATOM	318	O	MET	63	14.313	3.286	-12.463	1.00	27.31
ATOM	319	CB	MET	63	12.588	3.986	-9.753	1.00	19.12
ATOM	320	CG	MET	63	14.018	4.202	-9.335	1.00	21.76
ATOM	321	SD	MET	63	14.350	3.308	-7.827	1.00	25.88
ATOM	322	CE	MET	63	14.496	1.636	-8.499	1.00	22.73
ATOM	323	N	LEU	64	12.946	1.614	-11.842	1.00	18.80
ATOM	324	CA	LEU	64	13.771	0.544	-12.398	1.00	18.07
ATOM	325	C	LEU	64	13.683	0.510	-13.903	1.00	23.00
ATOM	326	O	LEU	64	14.634	0.119	-14.573	1.00	24.06
ATOM	327	CB	LEU	64	13.328	-0.814	-11.853	1.00	17.89
ATOM	328	CG	LEU	64	14.035	-2.059	-12.384	1.00	22.43
ATOM	329	CD1	LEU	64	15.469	-2.072	-11.924	1.00	22.35
ATOM	330	CD2	LEU	64	13.307	-3.307	-11.918	1.00	25.46
ATOM	331	N	SER	65	12.551	0.949	-14.437	1.00	20.59
ATOM	332	CA	SER	65	12.361	0.942	-15.874	1.00	20.79
ATOM	333	C	SER	65	13.360	1.880	-16.533	1.00	24.97
ATOM	334	O	SER	65	13.646	1.751	-17.716	1.00	26.49
ATOM	335	CB	SER	65	10.947	1.367	-16.230	1.00	24.46
ATOM	336	OG	SER	65	10.758	2.745	-15.960	1.00	37.12
ATOM	337	N	LEU	66	13.887	2.826	-15.763	1.00	18.20
ATOM	338	CA	LEU	66	14.848	3.781	-16.292	1.00	16.09
ATOM	339	C	LEU	66	16.145	3.084	-16.658	1.00	19.61
ATOM	340	O	LEU	66	16.942	3.621	-17.409	1.00	19.59
ATOM	341	CB	LEU	66	15.130	4.892	-15.274	1.00	15.19
ATOM	342	CG	LEU	66	13.921	5.676	-14.767	1.00	17.85
ATOM	343	CD1	LEU	66	14.335	6.635	-13.683	1.00	17.63
ATOM	344	CD2	LEU	66	13.251	6.396	-15.902	1.00	16.61
ATOM	345	N	GLY	67	16.370	1.904	-16.096	1.00	18.62

ATOM	346	CA	GLY	67	17.582	1.159	-16.384	1.00	19.69
ATOM	347	C	GLY	67	17.302	0.034	-17.361	1.00	25.74
ATOM	348	O	GLY	67	18.188	-0.756	-17.691	1.00	27.68
ATOM	349	N	THR	68	16.063	-0.038	-17.832	1.00	18.44
ATOM	350	CA	THR	68	15.677	-1.079	-18.769	1.00	15.20
ATOM	351	C	THR	68	15.511	-0.525	-20.177	1.00	16.21
ATOM	352	O	THR	68	15.277	0.671	-20.357	1.00	16.20
ATOM	353	CB	THR	68	14.367	-1.777	-18.321	1.00	10.45
ATOM	354	OG1	THR	68	13.305	-0.815	-18.219	1.00	9.49
ATOM	355	CG2	THR	68	14.557	-2.454	-16.987	1.00	1.57
ATOM	356	N	LYS	69	15.575	-1.408	-21.165	1.00	11.62
ATOM	357	CA	LYS	69	15.435	-1.009	-22.557	1.00	12.61
ATOM	358	C	LYS	69	14.490	-1.962	-23.291	1.00	20.44
ATOM	359	O	LYS	69	14.153	-3.029	-22.762	1.00	21.50
ATOM	360	CB	LYS	69	16.815	-1.000	-23.238	1.00	14.74
ATOM	361	CG	LYS	69	17.764	0.048	-22.676	1.00	30.38
ATOM	362	CD	LYS	69	19.066	0.138	-23.445	1.00	43.51
ATOM	363	CE	LYS	69	19.975	1.219	-22.860	1.00	64.68
ATOM	364	NZ	LYS	69	21.244	1.376	-23.619	1.00	74.82
ATOM	365	N	ALA	70	13.948	-1.521	-24.426	1.00	16.85
ATOM	366	CA	ALA	70	13.083	-2.372	-25.248	1.00	17.01
ATOM	367	C	ALA	70	11.969	-3.131	-24.526	1.00	21.95
ATOM	368	O	ALA	70	11.415	-2.636	-23.551	1.00	23.28
ATOM	369	CB	ALA	70	13.933	-3.341	-26.054	1.00	18.23
ATOM	370	N	ASP	71	11.653	-4.333	-25.010	1.00	18.01
ATOM	371	CA	ASP	71	10.585	-5.172	-24.451	1.00	18.92
ATOM	372	C	ASP	71	10.616	-5.216	-22.920	1.00	26.30
ATOM	373	O	ASP	71	9.603	-4.985	-22.263	1.00	27.15
ATOM	374	CB	ASP	71	10.672	-6.612	-24.988	1.00	22.13
ATOM	375	CG	ASP	71	10.770	-6.686	-26.513	1.00	51.31
ATOM	376	OD1	ASP	71	10.518	-5.694	-27.221	1.00	59.09
ATOM	377	OD2	ASP	71	11.099	-7.783	-27.013	1.00	60.06
ATOM	378	N	THR	72	11.812	-5.438	-22.371	1.00	24.21
ATOM	379	CA	THR	72	12.044	-5.535	-20.925	1.00	22.94
ATOM	380	C	THR	72	11.427	-4.353	-20.167	1.00	24.66
ATOM	381	O	THR	72	10.811	-4.517	-19.112	1.00	24.36
ATOM	382	CB	THR	72	13.569	-5.555	-20.653	1.00	29.44
ATOM	383	OG1	THR	72	14.173	-6.639	-21.376	1.00	30.43
ATOM	384	CG2	THR	72	13.862	-5.721	-19.167	1.00	28.97
ATOM	385	N	HIS	73	11.600	-3.172	-20.743	1.00	19.21
ATOM	386	CA	HIS	73	11.120	-1.931	-20.187	1.00	17.25
ATOM	387	C	HIS	73	9.629	-1.737	-20.394	1.00	24.90
ATOM	388	O	HIS	73	8.888	-1.507	-19.441	1.00	25.89
ATOM	389	CB	HIS	73	11.892	-0.798	-20.848	1.00	16.14
ATOM	390	CG	HIS	73	11.303	0.545	-20.624	1.00	18.99
ATOM	391	ND1	HIS	73	10.438	1.137	-21.525	1.00	21.51
ATOM	392	CD2	HIS	73	11.467	1.437	-19.622	1.00	21.38
ATOM	393	CE1	HIS	73	10.103	2.334	-21.083	1.00	21.60
ATOM	394	NE2	HIS	73	10.713	2.539	-19.936	1.00	21.99
ATOM	395	N	ASP	74	9.209	-1.800	-21.656	1.00	21.47
ATOM	396	CA	ASP	74	7.814	-1.609	-22.053	1.00	19.79
ATOM	397	C	ASP	74	6.922	-2.530	-21.279	1.00	21.39
ATOM	398	O	ASP	74	5.805	-2.167	-20.931	1.00	23.80
ATOM	399	CB	ASP	74	7.650	-1.873	-23.540	1.00	21.48

ATOM	400	CG	ASP	74	8.272	-0.790	-24.394	1.00	31.57
ATOM	401	OD1	ASP	74	8.786	0.212	-23.867	1.00	31.06
ATOM	402	OD2	ASP	74	8.230	-0.945	-25.629	1.00	42.19
ATOM	403	N	GLU	75	7.455	-3.702	-20.973	1.00	14.48
ATOM	404	CA	GLU	75	6.738	-4.701	-20.221	1.00	14.26
ATOM	405	C	GLU	75	6.482	-4.248	-18.788	1.00	20.06
ATOM	406	O	GLU	75	5.425	-4.543	-18.226	1.00	21.61
ATOM	407	CB	GLU	75	7.539	-5.989	-20.228	1.00	15.78
ATOM	408	CG	GLU	75	6.812	-7.174	-19.656	1.00	32.90
ATOM	409	CD	GLU	75	7.666	-8.413	-19.711	1.00	59.73
ATOM	410	OE1	GLU	75	8.603	-8.484	-18.886	1.00	56.25
ATOM	411	OE2	GLU	75	7.419	-9.301	-20.548	1.00	53.12
ATOM	412	N	ILE	76	7.445	-3.542	-18.196	1.00	15.73
ATOM	413	CA	ILE	76	7.290	-3.055	-16.828	1.00	15.03
ATOM	414	C	ILE	76	6.214	-1.984	-16.793	1.00	21.66
ATOM	415	O	ILE	76	5.222	-2.122	-16.079	1.00	22.85
ATOM	416	CB	ILE	76	8.614	-2.476	-16.251	1.00	17.25
ATOM	417	CG1	ILE	76	9.663	-3.582	-16.092	1.00	16.04
ATOM	418	CG2	ILE	76	8.362	-1.794	-14.914	1.00	17.21
ATOM	419	CD1	ILE	76	10.958	-3.133	-15.411	1.00	14.11
ATOM	420	N	LEU	77	6.382	-0.941	-17.599	1.00	16.68
ATOM	421	CA	LEU	77	5.406	0.148	-17.633	1.00	15.81
ATOM	422	C	LEU	77	4.007	-0.357	-17.981	1.00	19.88
ATOM	423	O	LEU	77	3.017	0.042	-17.370	1.00	19.28
ATOM	424	CB	LEU	77	5.839	1.252	-18.602	1.00	14.72
ATOM	425	CG	LEU	77	7.174	1.944	-18.299	1.00	19.72
ATOM	426	CD1	LEU	77	7.429	3.032	-19.319	1.00	20.78
ATOM	427	CD2	LEU	77	7.199	2.525	-16.901	1.00	17.87
ATOM	428	N	GLU	78	3.930	-1.264	-18.942	1.00	15.10
ATOM	429	CA	GLU	78	2.646	-1.819	-19.325	1.00	14.48
ATOM	430	C	GLU	78	2.115	-2.691	-18.194	1.00	15.59
ATOM	431	O	GLU	78	0.908	-2.773	-17.979	1.00	13.66
ATOM	432	CB	GLU	78	2.767	-2.619	-20.608	1.00	16.58
ATOM	433	CG	GLU	78	2.803	-1.805	-21.888	1.00	34.30
ATOM	434	CD	GLU	78	3.049	-2.682	-23.092	1.00	66.97
ATOM	435	OE1	GLU	78	2.677	-3.877	-23.057	1.00	63.59
ATOM	436	OE2	GLU	78	3.629	-2.174	-24.070	1.00	69.86
ATOM	437	N	GLY	79	3.027	-3.330	-17.471	1.00	14.27
ATOM	438	CA	GLY	79	2.649	-4.167	-16.341	1.00	16.07
ATOM	439	C	GLY	79	2.136	-3.316	-15.189	1.00	25.07
ATOM	440	O	GLY	79	1.340	-3.768	-14.357	1.00	27.66
ATOM	441	N	LEU	80	2.589	-2.066	-15.140	1.00	18.21
ATOM	442	CA	LEU	80	2.143	-1.135	-14.108	1.00	14.93
ATOM	443	C	LEU	80	0.880	-0.410	-14.555	1.00	13.69
ATOM	444	O	LEU	80	0.553	0.668	-14.054	1.00	9.47
ATOM	445	CB	LEU	80	3.227	-0.115	-13.769	1.00	14.43
ATOM	446	CG	LEU	80	4.536	-0.689	-13.241	1.00	17.68
ATOM	447	CD1	LEU	80	5.522	0.440	-13.082	1.00	17.74
ATOM	448	CD2	LEU	80	4.325	-1.444	-11.948	1.00	14.60
ATOM	449	N	ASN	81	0.160	-1.027	-15.481	1.00	13.09
ATOM	450	CA	ASN	81	-1.081	-0.470	-15.983	1.00	14.16
ATOM	451	C	ASN	81	-0.914	0.888	-16.674	1.00	18.30
ATOM	452	O	ASN	81	-1.660	1.831	-16.409	1.00	16.62
ATOM	453	CB	ASN	81	-2.106	-0.407	-14.846	1.00	17.98

ATOM	454	CG	ASN	81	-2.968	-1.649	-14.764	1.00 44.40
ATOM	455	OD1	ASN	81	-4.062	-1.682	-15.329	1.00 52.81
ATOM	456	ND2	ASN	81	-2.504	-2.668	-14.041	1.00 23.67
ATOM	457	N	PHE	82	0.056	0.954	-17.586	1.00 15.78
ATOM	458	CA	PHE	82	0.342	2.158	-18.353	1.00 15.33
ATOM	459	C	PHE	82	0.273	1.836	-19.838	1.00 23.98
ATOM	460	O	PHE	82	1.019	0.993	-20.342	1.00 27.23
ATOM	461	CB	PHE	82	1.729	2.725	-18.027	1.00 16.18
ATOM	462	CG	PHE	82	1.782	3.505	-16.746	1.00 17.62
ATOM	463	CD1	PHE	82	1.321	4.808	-16.694	1.00 18.51
ATOM	464	CD2	PHE	82	2.292	2.929	-15.584	1.00 21.78
ATOM	465	CE1	PHE	82	1.364	5.529	-15.502	1.00 21.96
ATOM	466	CE2	PHE	82	2.339	3.642	-14.386	1.00 22.22
ATOM	467	CZ	PHE	82	1.874	4.943	-14.343	1.00 20.41
ATOM	468	N	ASN	83	-0.634	2.502	-20.542	1.00 16.94
ATOM	469	CA	ASN	83	-0.785	2.291	-21.972	1.00 15.03
ATOM	470	C	ASN	83	0.244	3.141	-22.670	1.00 22.28
ATOM	471	O	ASN	83	-0.001	4.310	-22.979	1.00 24.99
ATOM	472	CB	ASN	83	-2.179	2.689	-22.429	1.00 16.41
ATOM	473	CG	ASN	83	-2.427	2.344	-23.868	1.00 38.32
ATOM	474	OD1	ASN	83	-1.513	1.946	-24.587	1.00 32.12
ATOM	475	ND2	ASN	83	-3.668	2.490	-24.303	1.00 35.98
ATOM	476	N	LEU	84	1.376	2.528	-22.978	1.00 17.89
ATOM	477	CA	LEU	84	2.474	3.248	-23.603	1.00 16.80
ATOM	478	C	LEU	84	2.171	3.967	-24.911	1.00 20.88
ATOM	479	O	LEU	84	2.840	4.945	-25.247	1.00 20.85
ATOM	480	CB	LEU	84	3.679	2.324	-23.764	1.00 15.58
ATOM	481	CG	LEU	84	4.156	1.723	-22.446	1.00 17.53
ATOM	482	CD1	LEU	84	5.318	0.790	-22.689	1.00 16.86
ATOM	483	CD2	LEU	84	4.522	2.829	-21.484	1.00 15.95
ATOM	484	N	THR	85	1.136	3.523	-25.610	1.00 18.16
ATOM	485	CA	THR	85	0.769	4.122	-26.884	1.00 19.35
ATOM	486	C	THR	85	-0.057	5.385	-26.715	1.00 22.48
ATOM	487	O	THR	85	-0.248	6.144	-27.658	1.00 22.41
ATOM	488	CB	THR	85	-0.018	3.131	-27.758	1.00 39.97
ATOM	489	OG1	THR	85	-1.145	2.622	-27.029	1.00 45.76
ATOM	490	CG2	THR	85	0.874	1.978	-28.176	1.00 40.70
ATOM	491	N	GLU	86	-0.544	5.613	-25.507	1.00 18.29
ATOM	492	CA	GLU	86	-1.367	6.777	-25.260	1.00 17.94
ATOM	493	C	GLU	86	-0.731	7.802	-24.354	1.00 19.87
ATOM	494	O	GLU	86	-1.012	8.991	-24.480	1.00 20.95
ATOM	495	CB	GLU	86	-2.721	6.348	-24.717	1.00 20.11
ATOM	496	CG	GLU	86	-3.508	5.480	-25.689	1.00 39.84
ATOM	497	CD	GLU	86	-4.902	5.171	-25.209	1.00 72.19
ATOM	498	OE1	GLU	86	-5.297	5.685	-24.141	1.00 63.51
ATOM	499	OE2	GLU	86	-5.598	4.403	-25.903	1.00 73.21
ATOM	500	N	ILE	87	0.152	7.357	-23.467	1.00 15.47
ATOM	501	CA	ILE	87	0.806	8.283	-22.547	1.00 16.06
ATOM	502	C	ILE	87	2.312	8.307	-22.730	1.00 21.27
ATOM	503	O	ILE	87	2.974	7.247	-22.757	1.00 21.63
ATOM	504	CB	ILE	87	0.446	8.004	-21.050	1.00 19.45
ATOM	505	CG1	ILE	87	1.034	9.101	-20.149	1.00 19.82
ATOM	506	CG2	ILE	87	0.925	6.624	-20.616	1.00 19.35
ATOM	507	CD1	ILE	87	0.602	9.016	-18.693	1.00 34.75

ATOM	508	N	PRO	88	2.868	9.508	-22.968	1.00	16.18
ATOM	509	CA	PRO	88	4.310	9.634	-23.152	1.00	15.24
ATOM	510	C	PRO	88	5.024	9.177	-21.886	1.00	18.67
ATOM	511	O	PRO	88	4.678	9.590	-20.783	1.00	17.17
ATOM	512	CB	PRO	88	4.522	11.127	-23.440	1.00	16.75
ATOM	513	CG	PRO	88	3.199	11.797	-23.254	1.00	21.07
ATOM	514	CD	PRO	88	2.149	10.739	-23.333	1.00	16.27
ATOM	515	N	GLU	89	6.034	8.331	-22.050	1.00	16.19
ATOM	516	CA	GLU	89	6.781	7.818	-20.908	1.00	16.21
ATOM	517	C	GLU	89	7.333	8.949	-20.063	1.00	22.88
ATOM	518	O	GLU	89	7.497	8.823	-18.842	1.00	22.93
ATOM	519	CB	GLU	89	7.892	6.896	-21.365	1.00	17.75
ATOM	520	CG	GLU	89	7.401	5.618	-22.033	1.00	34.85
ATOM	521	CD	GLU	89	8.539	4.728	-22.483	1.00	61.89
ATOM	522	OE1	GLU	89	9.710	5.040	-22.159	1.00	48.17
ATOM	523	OE2	GLU	89	8.262	3.710	-23.154	1.00	62.54
ATOM	524	N	ALA	90	7.636	10.052	-20.731	1.00	20.84
ATOM	525	CA	ALA	90	8.156	11.236	-20.062	1.00	20.22
ATOM	526	C	ALA	90	7.146	11.696	-19.016	1.00	22.01
ATOM	527	O	ALA	90	7.525	12.203	-17.963	1.00	19.24
ATOM	528	CB	ALA	90	8.392	12.343	-21.082	1.00	21.10
ATOM	529	N	GLN	91	5.864	11.486	-19.316	1.00	19.33
ATOM	530	CA	GLN	91	4.773	11.860	-18.430	1.00	19.39
ATOM	531	C	GLN	91	4.609	10.862	-17.306	1.00	23.78
ATOM	532	O	GLN	91	4.231	11.239	-16.197	1.00	24.85
ATOM	533	CB	GLN	91	3.452	12.006	-19.184	1.00	20.95
ATOM	534	CG	GLN	91	3.195	13.409	-19.735	1.00	48.56
ATOM	535	CD	GLN	91	1.749	13.610	-20.170	1.00	73.81
ATOM	536	OE1	GLN	91	0.907	12.724	-20.002	1.00	69.27
ATOM	537	NE2	GLN	91	1.455	14.776	-20.732	1.00	63.27
ATOM	538	N	ILE	92	4.932	9.603	-17.578	1.00	17.45
ATOM	539	CA	ILE	92	4.823	8.557	-16.563	1.00	15.82
ATOM	540	C	ILE	92	5.773	8.855	-15.422	1.00	21.60
ATOM	541	O	ILE	92	5.363	8.946	-14.272	1.00	22.63
ATOM	542	CB	ILE	92	5.160	7.164	-17.136	1.00	17.45
ATOM	543	CG1	ILE	92	4.097	6.754	-18.160	1.00	17.24
ATOM	544	CG2	ILE	92	5.295	6.150	-16.015	1.00	16.93
ATOM	545	CD1	ILE	92	4.330	5.414	-18.814	1.00	23.97
ATOM	546	N	HIS	93	7.035	9.082	-15.763	1.00	17.87
ATOM	547	CA	HIS	93	8.055	9.374	-14.763	1.00	16.61
ATOM	548	C	HIS	93	7.815	10.736	-14.113	1.00	21.94
ATOM	549	O	HIS	93	7.971	10.877	-12.904	1.00	21.04
ATOM	550	CB	HIS	93	9.449	9.289	-15.385	1.00	16.45
ATOM	551	CG	HIS	93	9.768	7.933	-15.949	1.00	19.48
ATOM	552	ND1	HIS	93	9.691	6.775	-15.205	1.00	21.37
ATOM	553	CD2	HIS	93	10.138	7.557	-17.191	1.00	21.86
ATOM	554	CE1	HIS	93	9.994	5.737	-15.962	1.00	21.40
ATOM	555	NE2	HIS	93	10.271	6.186	-17.177	1.00	22.02
ATOM	556	N	GLU	94	7.382	11.720	-14.901	1.00	21.50
ATOM	557	CA	GLU	94	7.111	13.062	-14.370	1.00	21.71
ATOM	558	C	GLU	94	5.996	12.961	-13.338	1.00	27.52
ATOM	559	O	GLU	94	6.059	13.576	-12.272	1.00	29.26
ATOM	560	CB	GLU	94	6.704	14.023	-15.488	1.00	23.76
ATOM	561	CG	GLU	94	6.268	15.417	-15.028	1.00	46.66

ATOM	562	CD	GLU	94	5.732	16.286	-16.166	1.00100.99
ATOM	563	OE1	GLU	94	5.513	15.769	-17.285	1.00110.00
ATOM	564	OE2	GLU	94	5.517	17.493	-15.933	1.00109.77
ATOM	565	N	GLY	95	5.015	12.116	-13.632	1.00 22.71
ATOM	566	CA	GLY	95	3.903	11.932	-12.723	1.00 21.91
ATOM	567	C	GLY	95	4.352	11.312	-11.407	1.00 26.12
ATOM	568	O	GLY	95	3.928	11.757	-10.337	1.00 26.39
ATOM	569	N	PHE	96	5.247	10.324	-11.477	1.00 20.03
ATOM	570	CA	PHE	96	5.755	9.640	-10.283	1.00 17.73
ATOM	571	C	PHE	96	6.559	10.556	-9.384	1.00 23.93
ATOM	572	O	PHE	96	6.513	10.436	-8.165	1.00 24.37
ATOM	573	CB	PHE	96	6.598	8.413	-10.656	1.00 18.46
ATOM	574	CG	PHE	96	5.784	7.171	-10.895	1.00 19.16
ATOM	575	CD1	PHE	96	5.127	6.543	-9.838	1.00 23.98
ATOM	576	CD2	PHE	96	5.627	6.655	-12.172	1.00 19.50
ATOM	577	CE1	PHE	96	4.323	5.420	-10.057	1.00 24.57
ATOM	578	CE2	PHE	96	4.825	5.534	-12.397	1.00 22.76
ATOM	579	CZ	PHE	96	4.174	4.920	-11.339	1.00 21.77
ATOM	580	N	GLN	97	7.273	11.493	-9.994	1.00 20.80
ATOM	581	CA	GLN	97	8.085	12.438	-9.254	1.00 19.78
ATOM	582	C	GLN	97	7.180	13.352	-8.453	1.00 21.06
ATOM	583	O	GLN	97	7.410	13.575	-7.267	1.00 19.65
ATOM	584	CB	GLN	97	8.961	13.243	-10.212	1.00 21.62
ATOM	585	CG	GLN	97	10.039	12.401	-10.901	1.00 53.46
ATOM	586	CD	GLN	97	10.845	13.187	-11.912	1.00 97.50
ATOM	587	OE1	GLN	97	10.669	14.400	-12.070	1.00102.38
ATOM	588	NE2	GLN	97	11.729	12.499	-12.616	1.00 92.80
ATOM	589	N	GLU	98	6.099	13.804	-9.078	1.00 18.84
ATOM	590	CA	GLU	98	5.156	14.693	-8.398	1.00 20.12
ATOM	591	C	GLU	98	4.676	14.065	-7.090	1.00 27.71
ATOM	592	O	GLU	98	4.631	14.715	-6.035	1.00 29.41
ATOM	593	CB	GLU	98	3.927	14.991	-9.276	1.00 21.69
ATOM	594	CG	GLU	98	4.158	15.965	-10.419	1.00 43.54
ATOM	595	CD	GLU	98	4.424	17.394	-9.964	1.00 92.78
ATOM	596	OE1	GLU	98	4.622	17.646	-8.753	1.00 95.84
ATOM	597	OE2	GLU	98	4.448	18.275	-10.845	1.00103.56
ATOM	598	N	LEU	99	4.384	12.775	-7.171	1.00 21.26
ATOM	599	CA	LEU	99	3.893	11.999	-6.053	1.00 19.05
ATOM	600	C	LEU	99	4.910	11.927	-4.934	1.00 24.77
ATOM	601	O	LEU	99	4.587	12.186	-3.771	1.00 24.94
ATOM	602	CB	LEU	99	3.552	10.599	-6.541	1.00 18.47
ATOM	603	CG	LEU	99	2.828	9.714	-5.548	1.00 23.63
ATOM	604	CD1	LEU	99	1.698	10.478	-4.922	1.00 23.11
ATOM	605	CD2	LEU	99	2.360	8.461	-6.253	1.00 27.37
ATOM	506	N	LEU	100	6.155	11.657	-5.303	1.00 21.61
ATOM	607	CA	LEU	100	7.240	11.541	-4.331	1.00 20.15
ATOM	608	C	LEU	100	7.551	12.896	-3.703	1.00 23.60
ATOM	609	O	LEU	100	7.939	12.970	-2.540	1.00 21.36
ATOM	610	CB	LEU	100	8.491	10.962	-5.006	1.00 20.24
ATOM	611	CG	LEU	100	8.299	9.633	-5.750	1.00 25.35
ATOM	612	CD1	LEU	100	9.589	9.234	-6.433	1.00 26.21
ATOM	613	CD2	LEU	100	7.823	8.558	-4.797	1.00 26.62
ATOM	614	N	ARG	101	7.259	13.960	-4.453	1.00 24.56
ATOM	615	CA	ARG	101	7.494	15.338	-4.019	1.00 26.50

ATOM	616	C	ARG	101	6.535	15.594	-2.869	1.00	29.95
ATOM	617	O	ARG	101	6.894	16.189	-1.840	1.00	29.61
ATOM	618	CB	ARG	101	7.196	16.303	-5.172	1.00	31.10
ATOM	619	CG	ARG	101	7.540	17.759	-4.904	1.00	50.33
ATOM	620	CD	ARG	101	6.916	18.678	-5.963	1.00	78.18
ATOM	621	NE	ARG	101	6.993	20.088	-5.582	1.00	97.33
ATOM	622	CZ	ARG	101	6.475	20.588	-4.462	1.00	110.00
ATOM	623	NH1	ARG	101	5.838	19.798	-3.606	1.00	109.24
ATOM	624	NH2	ARG	101	6.619	21.876	-4.183	1.00	98.32
ATOM	625	N	THR	102	5.322	15.087	-3.046	1.00	26.75
ATOM	626	CA	THR	102	4.297	15.221	-2.042	1.00	27.11
ATOM	627	C	THR	102	4.624	14.273	-0.900	1.00	31.26
ATOM	628	O	THR	102	4.400	14.585	0.236	1.00	34.20
ATOM	629	CB	THR	102	2.907	14.861	-2.598	1.00	46.57
ATOM	630	OG1	THR	102	2.619	15.665	-3.757	1.00	50.68
ATOM	631	CG2	THR	102	1.841	15.098	-1.543	1.00	50.86
ATOM	632	N	LEU	103	5.202	13.122	-1.176	1.00	24.28
ATOM	633	CA	LEU	103	5.490	12.223	-0.080	1.00	21.81
ATOM	634	C	LEU	103	6.731	12.644	0.744	1.00	28.18
ATOM	635	O	LEU	103	6.821	12.344	1.943	1.00	27.87
ATOM	636	CB	LEU	103	5.573	10.784	-0.605	1.00	20.79
ATOM	637	CG	LEU	103	4.304	10.284	-1.322	1.00	24.82
ATOM	638	CD1	LEU	103	4.471	8.845	-1.787	1.00	25.29
ATOM	639	CD2	LEU	103	3.104	10.398	-0.409	1.00	25.55
ATOM	640	N	ASN	104	7.657	13.385	0.127	1.00	26.19
ATOM	641	CA	ASN	104	8.876	13.829	0.822	1.00	26.92
ATOM	642	C	ASN	104	8.494	14.854	1.879	1.00	29.91
ATOM	643	O	ASN	104	8.663	14.622	3.077	1.00	30.79
ATOM	644	CB	ASN	104	9.890	14.438	-0.156	1.00	33.86
ATOM	645	CG	ASN	104	11.321	13.946	0.087	1.00	67.01
ATOM	646	OD1	ASN	104	12.120	13.843	-0.853	1.00	64.96
ATOM	647	ND2	ASN	104	11.647	13.632	1.341	1.00	57.77
ATOM	648	N	GLN	105	7.999	15.994	1.419	1.00	25.50
ATOM	649	CA	GLN	105	7.532	17.062	2.315	1.00	24.94
ATOM	650	C	GLN	105	6.172	17.475	1.746	1.00	28.97
ATOM	651	O	GLN	105	6.061	18.452	0.978	1.00	31.34
ATOM	652	CB	GLN	105	8.540	18.227	2.379	1.00	26.65
ATOM	653	CG	GLN	105	8.082	19.454	3.220	1.00	66.64
ATOM	654	CD	GLN	105	7.531	19.104	4.601	1.00	105.25
ATOM	655	OE1	GLN	105	7.741	18.003	5.110	1.00	107.04
ATOM	656	NE2	GLN	105	6.794	20.042	5.200	1.00	99.00
ATOM	657	N	PRO	106	5.125	16.697	2.076	1.00	20.86
ATOM	658	CA	PRO	106	3.741	16.897	1.634	1.00	18.74
ATOM	659	C	PRO	106	3.006	18.152	2.061	1.00	22.19
ATOM	660	O	PRO	106	3.582	19.222	2.292	1.00	21.82
ATOM	661	CB	PRO	106	3.007	15.630	2.128	1.00	19.72
ATOM	662	CG	PRO	106	3.863	15.067	3.172	1.00	24.39
ATOM	663	CD	PRO	106	5.271	15.488	2.912	1.00	20.20
ATOM	664	N	ASP	107	1.686	17.981	2.058	1.00	18.09
ATOM	665	CA	ASP	107	0.701	18.968	2.471	1.00	17.45
ATOM	666	C	ASP	107	0.623	18.789	3.996	1.00	21.97
ATOM	667	O	ASP	107	-0.182	19.441	4.670	1.00	21.75
ATOM	668	CB	ASP	107	-0.637	18.596	1.818	1.00	18.93
ATOM	669	CG	ASP	107	-1.728	19.659	1.968	1.00	27.12

ATOM	670	OD1	ASP	107	-1.630	20.613	2.757	1.00	27.68
ATOM	671	OD2	ASP	107	-2.746	19.503	1.264	1.00	32.41
ATOM	672	N	SER	108	1.516	17.945	4.522	1.00	18.59
ATOM	673	CA	SER	108	1.615	17.640	5.945	1.00	18.81
ATOM	674	C	SER	108	2.474	16.396	6.169	1.00	24.34
ATOM	675	O	SER	108	2.385	15.429	5.416	1.00	23.92
ATOM	676	CB	SER	108	0.225	17.412	6.549	1.00	22.39
ATOM	677	OG	SER	108	0.291	17.068	7.921	1.00	30.77
ATOM	678	N	GLN	109	3.269	16.416	7.230	1.00	22.70
ATOM	679	CA	GLN	109	4.127	15.294	7.567	1.00	22.48
ATOM	680	C	GLN	109	3.261	14.181	8.176	1.00	28.45
ATOM	681	O	GLN	109	2.765	14.282	9.305	1.00	29.12
ATOM	682	CB	GLN	109	5.228	15.755	8.528	1.00	23.92
ATOM	683	CG	GLN	109	6.103	14.639	9.058	1.00	60.78
ATOM	684	CD	GLN	109	7.177	15.138	10.006	1.00	102.33
ATOM	685	OE1	GLN	109	7.171	16.298	10.434	1.00	99.17
ATOM	686	NE2	GLN	109	8.106	14.257	10.346	1.00	106.94
ATOM	687	N	LEU	110	3.019	13.171	7.352	1.00	23.12
ATOM	688	CA	LEU	110	2.253	11.985	7.702	1.00	21.02
ATOM	689	C	LEU	110	3.304	10.897	7.951	1.00	26.33
ATOM	690	O	LEU	110	4.126	10.628	7.070	1.00	25.47
ATOM	691	CB	LEU	110	1.397	11.615	6.494	1.00	20.21
ATOM	692	CG	LEU	110	0.740	10.249	6.412	1.00	25.95
ATOM	693	CD1	LEU	110	-0.593	10.264	7.141	1.00	26.79
ATOM	694	CD2	LEU	110	0.542	9.904	4.949	1.00	28.71
ATOM	695	N	GLN	111	3.329	10.300	9.143	1.00	24.86
ATOM	696	CA	GLN	111	4.340	9.272	9.397	1.00	25.38
ATOM	697	C	GLN	111	4.256	8.154	8.383	1.00	30.55
ATOM	698	O	GLN	111	3.314	7.360	8.388	1.00	32.78
ATOM	699	CB	GLN	111	4.271	8.702	10.819	1.00	27.74
ATOM	700	CG	GLN	111	4.825	9.658	11.876	1.00	70.63
ATOM	701	CD	GLN	111	5.296	8.965	13.140	1.00	107.33
ATOM	702	OE1	GLN	111	5.247	7.736	13.265	1.00	106.26
ATOM	703	NE2	GLN	111	5.787	9.758	14.081	1.00	107.12
ATOM	704	N	LEU	112	5.222	8.154	7.477	1.00	22.86
ATOM	705	CA	LEU	112	5.289	7.152	6.441	1.00	20.43
ATOM	706	C	LEU	112	6.746	6.771	6.330	1.00	27.64
ATOM	707	O	LEU	112	7.605	7.617	6.082	1.00	31.14
ATOM	708	CB	LEU	112	4.786	7.712	5.108	1.00	19.99
ATOM	709	CG	LEU	112	4.265	6.699	4.092	1.00	25.35
ATOM	710	CD1	LEU	112	3.255	5.811	4.769	1.00	27.10
ATOM	711	CD2	LEU	112	3.631	7.405	2.930	1.00	27.66
ATOM	712	N	THR	113	7.022	5.500	6.569	1.00	22.74
ATOM	713	CA	THR	113	8.377	4.992	6.497	1.00	21.64
ATOM	714	C	THR	113	8.426	4.105	5.263	1.00	22.88
ATOM	715	O	THR	113	8.173	2.903	5.349	1.00	24.09
ATOM	716	CB	THR	113	8.693	4.173	7.744	1.00	31.66
ATOM	717	OG1	THR	113	8.266	4.902	8.901	1.00	32.16
ATOM	718	CG2	THR	113	10.178	3.922	7.843	1.00	32.13
ATOM	719	N	THR	114	8.755	4.699	4.121	1.00	16.81
ATOM	720	CA	THR	114	8.790	3.956	2.875	1.00	17.52
ATOM	721	C	THR	114	10.154	4.090	2.247	1.00	23.76
ATOM	722	O	THR	114	10.800	5.126	2.394	1.00	26.47
ATOM	723	CB	THR	114	7.757	4.503	1.897	1.00	30.93

ATOM	724	OG1	THR	114	6.481	4.563	2.551	1.00	42.28
ATOM	725	CG2	THR	114	7.663	3.621	0.647	1.00	27.57
ATOM	726	N	GLY	115	10.598	3.053	1.550	1.00	16.87
ATOM	727	CA	GLY	115	11.891	3.139	0.926	1.00	15.61
ATOM	728	C	GLY	115	12.062	2.062	-0.098	1.00	17.27
ATOM	729	O	GLY	115	11.266	1.133	-0.168	1.00	15.25
ATOM	730	N	ASN	116	13.091	2.201	-0.916	1.00	14.85
ATOM	731	CA	ASN	116	13.362	1.224	-1.938	1.00	15.66
ATOM	732	C	ASN	116	14.855	1.125	-1.986	1.00	22.82
ATOM	733	O	ASN	116	15.540	2.139	-2.127	1.00	24.97
ATOM	734	CB	ASN	116	12.841	1.707	-3.288	1.00	15.07
ATOM	735	CG	ASN	116	12.611	0.571	-4.262	1.00	32.48
ATOM	736	OD1	ASN	116	11.539	-0.044	-4.302	1.00	19.35
ATOM	737	ND2	ASN	116	13.635	0.269	-5.040	1.00	26.27
ATOM	738	N	GLY	117	15.362	-0.071	-1.725	1.00	18.70
ATOM	739	CA	GLY	117	16.793	-0.279	-1.766	1.00	18.14
ATOM	740	C	GLY	117	17.191	-1.264	-2.837	1.00	19.98
ATOM	741	O	GLY	117	16.601	-2.334	-2.966	1.00	19.82
ATOM	742	N	LEU	118	18.142	-0.863	-3.664	1.00	16.87
ATOM	743	CA	LEU	118	18.639	-1.733	-4.718	1.00	18.55
ATOM	744	C	LEU	118	19.993	-2.254	-4.269	1.00	23.29
ATOM	745	O	LEU	118	20.739	-1.547	-3.596	1.00	24.97
ATOM	746	CB	LEU	118	18.789	-0.962	-6.031	1.00	19.98
ATOM	747	CG	LEU	118	17.502	-0.316	-6.544	1.00	28.09
ATOM	748	CD1	LEU	118	17.780	0.426	-7.840	1.00	29.68
ATOM	749	CD2	LEU	118	16.424	-1.371	-6.744	1.00	32.51
ATOM	750	N	PHE	119	20.280	-3.506	-4.593	1.00	17.89
ATOM	751	CA	PHE	119	21.541	-4.126	-4.210	1.00	16.32
ATOM	752	C	PHE	119	22.134	-4.817	-5.418	1.00	22.19
ATOM	753	O	PHE	119	21.631	-5.857	-5.855	1.00	22.47
ATOM	754	CB	PHE	119	21.313	-5.145	-3.095	1.00	17.42
ATOM	755	CG	PHE	119	20.615	-4.580	-1.895	1.00	19.13
ATOM	756	CD1	PHE	119	19.225	-4.559	-1.835	1.00	22.10
ATOM	757	CD2	PHE	119	21.343	-4.032	-0.838	1.00	21.73
ATOM	758	CE1	PHE	119	18.562	-3.997	-0.742	1.00	23.31
ATOM	759	CE2	PHE	119	20.690	-3.465	0.265	1.00	24.31
ATOM	760	CZ	PHE	119	19.295	-3.447	0.312	1.00	21.97
ATOM	761	N	LEU	120	23.187	-4.228	-5.970	1.00	18.38
ATOM	762	CA	LEU	120	23.844	-4.781	-7.143	1.00	18.54
ATOM	763	C	LEU	120	25.235	-5.300	-6.786	1.00	22.11
ATOM	764	O	LEU	120	25.877	-4.822	-5.850	1.00	22.69
ATOM	765	CB	LEU	120	23.940	-3.719	-8.240	1.00	19.33
ATOM	766	CG	LEU	120	22.655	-3.047	-8.732	1.00	24.92
ATOM	767	CD1	LEU	120	22.103	-2.051	-7.721	1.00	26.07
ATOM	768	CD2	LEU	120	22.979	-2.335	-10.008	1.00	28.44
ATOM	769	N	SER	121	25.702	-6.272	-7.556	1.00	16.99
ATOM	770	CA	SER	121	26.993	-6.894	-7.319	1.00	16.93
ATOM	771	C	SER	121	28.199	-5.956	-7.334	1.00	23.52
ATOM	772	O	SER	121	28.300	-5.060	-8.172	1.00	25.92
ATOM	773	CB	SER	121	27.198	-8.031	-8.324	1.00	19.90
ATOM	774	OG	SER	121	28.428	-8.698	-8.114	1.00	30.55
ATOM	775	N	GLU	122	29.083	-6.124	-6.355	1.00	19.64
ATOM	776	CA	GLU	122	30.323	-5.351	-6.313	1.00	19.06
ATOM	777	C	GLU	122	31.114	-5.991	-7.452	1.00	22.25

ATOM	778	O	GLU	122	31.417	-7.182	-7.415	1.00	22.67
ATOM	779	CB	GLU	122	31.073	-5.563	-4.991	1.00	20.98
ATOM	780	CG	GLU	122	30.907	-4.444	-3.958	1.00	39.74
ATOM	781	CD	GLU	122	31.566	-4.756	-2.618	1.00	71.75
ATOM	782	OE1	GLU	122	31.886	-5.935	-2.354	1.00	64.09
ATOM	783	OE2	GLU	122	31.753	-3.819	-1.818	1.00	68.63
ATOM	784	N	GLY	123	31.369	-5.223	-8.497	1.00	18.92
ATOM	785	CA	GLY	123	32.095	-5.750	-9.637	1.00	19.03
ATOM	786	C	GLY	123	31.430	-5.342	-10.937	1.00	24.70
ATOM	787	O	GLY	123	32.028	-5.437	-12.005	1.00	25.16
ATOM	788	N	LEU	124	30.169	-4.931	-10.859	1.00	19.85
ATOM	789	CA	LEU	124	29.457	-4.493	-12.048	1.00	18.58
ATOM	790	C	LEU	124	29.702	-2.997	-12.249	1.00	21.59
ATOM	791	O	LEU	124	29.545	-2.205	-11.318	1.00	20.17
ATOM	792	CB	LEU	124	27.950	-4.777	-11.928	1.00	17.99
ATOM	793	CG	LEU	124	27.479	-6.233	-11.813	1.00	22.20
ATOM	794	CD1	LEU	124	25.964	-6.268	-11.773	1.00	21.86
ATOM	795	CD2	LEU	124	28.003	-7.073	-12.962	1.00	25.97
ATOM	796	N	LYS	125	30.131	-2.625	-13.451	1.00	18.27
ATOM	797	CA	LYS	125	30.384	-1.228	-13.756	1.00	19.18
ATOM	798	C	LYS	125	29.060	-0.571	-14.105	1.00	26.77
ATOM	799	O	LYS	125	28.658	-0.505	-15.271	1.00	28.15
ATOM	800	CB	LYS	125	31.384	-1.081	-14.901	1.00	22.19
ATOM	801	CG	LYS	125	31.786	0.355	-15.201	1.00	48.12
ATOM	802	CD	LYS	125	32.644	0.417	-16.452	1.00	72.20
ATOM	803	CE	LYS	125	32.959	1.843	-16.856	1.00	97.06
ATOM	804	NZ	LYS	125	31.717	2.597	-17.188	1.00	110.00
ATOM	805	N	LEU	126	28.342	-0.187	-13.059	1.00	20.76
ATOM	806	CA	LEU	126	27.043	0.457	-13.191	1.00	19.13
ATOM	807	C	LEU	126	27.091	1.792	-13.928	1.00	20.04
ATOM	808	O	LEU	126	28.085	2.524	-13.858	1.00	19.63
ATOM	809	CB	LEU	126	26.416	0.666	-11.808	1.00	18.62
ATOM	810	CG	LEU	126	26.553	-0.471	-10.794	1.00	22.87
ATOM	811	CD1	LEU	126	25.839	-0.077	-9.531	1.00	23.68
ATOM	812	CD2	LEU	126	26.012	-1.765	-11.344	1.00	24.83
ATOM	813	N	VAL	127	25.995	2.109	-14.609	1.00	16.04
ATOM	814	CA	VAL	127	25.861	3.348	-15.356	1.00	16.40
ATOM	815	C	VAL	127	25.538	4.485	-14.392	1.00	22.64
ATOM	816	O	VAL	127	24.529	4.463	-13.696	1.00	24.15
ATOM	817	CB	VAL	127	24.759	3.223	-16.409	1.00	20.46
ATOM	818	CG1	VAL	127	24.518	4.554	-17.101	1.00	21.01
ATOM	819	CG2	VAL	127	25.139	2.149	-17.423	1.00	20.09
ATOM	820	N	ASP	128	26.391	5.497	-14.367	1.00	19.51
ATOM	821	CA	ASP	128	26.211	6.629	-13.468	1.00	19.12
ATOM	822	C	ASP	128	24.851	7.287	-13.620	1.00	23.48
ATOM	823	O	ASP	128	24.201	7.600	-12.630	1.00	24.08
ATOM	824	CB	ASP	128	27.329	7.645	-13.675	1.00	21.97
ATOM	825	CG	ASP	128	28.701	7.022	-13.525	1.00	44.91
ATOM	826	OD1	ASP	128	29.016	6.487	-12.448	1.00	47.60
ATOM	827	OD2	ASP	128	29.467	7.052	-14.519	1.00	53.48
ATOM	828	N	LYS	129	24.387	7.404	-14.859	1.00	19.51
ATOM	829	CA	LYS	129	23.096	8.035	-15.126	1.00	18.71
ATOM	830	C	LYS	129	21.985	7.373	-14.334	1.00	23.17
ATOM	831	O	LYS	129	21.214	8.051	-13.663	1.00	24.46

ATOM	832	CB	LYS	129	22.786	8.008	-16.625	1.00	20.79
ATOM	833	CG	LYS	129	21.453	8.643	-16.990	1.00	25.39
ATOM	834	CD	LYS	129	21.325	10.074	-16.495	1.00	29.03
ATOM	835	CE	LYS	129	19.942	10.622	-16.783	1.00	32.86
ATOM	836	NZ	LYS	129	19.805	12.052	-16.436	1.00	32.94
ATOM	837	N	PHE	130	21.941	6.048	-14.370	1.00	18.58
ATOM	838	CA	PHE	130	20.915	5.316	-13.649	1.00	17.25
ATOM	839	C	PHE	130	20.988	5.613	-12.162	1.00	24.40
ATOM	840	O	PHE	130	19.966	5.911	-11.540	1.00	26.31
ATOM	841	CB	PHE	130	21.041	3.819	-13.902	1.00	17.61
ATOM	842	CG	PHE	130	20.051	2.988	-13.133	1.00	18.20
ATOM	843	CD1	PHE	130	18.689	3.105	-13.383	1.00	21.03
ATOM	844	CD2	PHE	130	20.480	2.098	-12.150	1.00	20.19
ATOM	845	CE1	PHE	130	17.775	2.355	-12.677	1.00	21.90
ATOM	846	CE2	PHE	130	19.574	1.344	-11.439	1.00	23.14
ATOM	847	CZ	PHE	130	18.218	1.471	-11.701	1.00	22.03
ATOM	848	N	LEU	131	22.198	5.583	-11.607	1.00	19.33
ATOM	849	CA	LEU	131	22.390	5.869	-10.183	1.00	18.53
ATOM	850	C	LEU	131	21.960	7.302	-9.851	1.00	24.96
ATOM	851	O	LEU	131	21.547	7.597	-8.726	1.00	25.24
ATOM	852	CB	LEU	131	23.840	5.617	-9.781	1.00	18.23
ATOM	853	CG	LEU	131	24.277	4.168	-10.024	1.00	23.10
ATOM	854	CD1	LEU	131	25.721	3.969	-9.608	1.00	23.85
ATOM	855	CD2	LEU	131	23.369	3.231	-9.259	1.00	24.10
ATOM	856	N	GLU	132	22.032	8.174	-10.851	1.00	21.30
ATOM	857	CA	GLU	132	21.603	9.555	-10.706	1.00	20.49
ATOM	858	C	GLU	132	20.089	9.531	-10.532	1.00	23.24
ATOM	859	O	GLU	132	19.558	10.012	-9.534	1.00	23.12
ATOM	860	CB	GLU	132	21.938	10.364	-11.964	1.00	22.47
ATOM	861	CG	GLU	132	23.416	10.574	-12.279	1.00	39.53
ATOM	862	CD	GLU	132	23.628	11.388	-13.548	1.00	72.71
ATOM	863	OE1	GLU	132	22.636	11.914	-14.100	1.00	55.71
ATOM	864	OE2	GLU	132	24.788	11.497	-13.995	1.00	75.11
ATOM	865	N	ASP	133	19.420	8.927	-11.510	1.00	19.34
ATOM	866	CA	ASP	133	17.958	8.794	-11.556	1.00	19.85
ATOM	867	C	ASP	133	17.394	8.128	-10.303	1.00	23.58
ATOM	868	O	ASP	133	16.344	8.517	-9.793	1.00	25.19
ATOM	869	CB	ASP	133	17.543	7.994	-12.793	1.00	22.71
ATOM	870	CG	ASP	133	17.978	8.655	-14.102	1.00	34.26
ATOM	871	OD1	ASP	133	18.560	9.760	-14.100	1.00	34.70
ATOM	872	OD2	ASP	133	17.719	8.036	-15.158	1.00	38.49
ATOM	873	N	VAL	134	18.110	7.126	-9.806	1.00	17.79
ATOM	874	CA	VAL	134	17.694	6.420	-8.605	1.00	17.47
ATOM	875	C	VAL	134	17.727	7.372	-7.397	1.00	24.76
ATOM	876	O	VAL	134	16.676	7.667	-6.829	1.00	24.51
ATOM	877	CB	VAL	134	18.576	5.171	-8.358	1.00	19.79
ATOM	878	CG1	VAL	134	18.265	4.560	-7.010	1.00	18.82
ATOM	879	CG2	VAL	134	18.343	4.151	-9.454	1.00	19.60
ATOM	880	N	LYS	135	18.902	7.940	-7.106	1.00	22.54
ATOM	881	CA	LYS	135	19.086	8.846	-5.965	1.00	22.49
ATOM	882	C	LYS	135	18.350	10.174	-6.089	1.00	26.45
ATOM	883	O	LYS	135	17.578	10.556	-5.201	1.00	27.66
ATOM	884	CB	LYS	135	20.573	9.123	-5.734	1.00	25.09
ATOM	885	CG	LYS	135	21.253	8.129	-4.805	1.00	41.63

ATOM	886	CD	LYS	135	21.299	6.711	-5.371	1.00	45.73
ATOM	887	CE	LYS	135	21.886	5.750	-4.341	1.00	58.07
ATOM	888	NZ	LYS	135	21.078	5.726	-3.078	1.00	74.45
ATOM	889	N	LYS	136	18.669	10.916	-7.141	1.00	21.97
ATOM	890	CA	LYS	136	18.044	12.207	-7.389	1.00	22.48
ATOM	891	C	LYS	136	16.573	12.089	-7.757	1.00	26.04
ATOM	892	O	LYS	136	15.709	12.328	-6.918	1.00	27.39
ATOM	893	CB	LYS	136	18.784	12.981	-8.478	1.00	27.45
ATOM	894	CG	LYS	136	20.077	13.637	-8.010	1.00	57.41
ATOM	895	CD	LYS	136	20.843	14.190	-9.193	1.00	70.91
ATOM	896	CE	LYS	136	21.349	13.048	-10.055	1.00	78.67
ATOM	897	NZ	LYS	136	21.862	13.453	-11.389	1.00	83.40
ATOM	898	N	LEU	137	16.289	11.710	-9.001	1.00	19.69
ATOM	899	CA	LEU	137	14.911	11.590	-9.460	1.00	18.86
ATOM	900	C	LEU	137	13.965	10.854	-8.512	1.00	25.85
ATOM	901	O	LEU	137	13.037	11.462	-7.987	1.00	31.02
ATOM	902	CB	LEU	137	14.837	10.940	-10.842	1.00	18.94
ATOM	903	CG	LEU	137	15.392	11.723	-12.026	1.00	25.53
ATOM	904	CD1	LEU	137	15.075	10.950	-13.276	1.00	26.83
ATOM	905	CD2	LEU	137	14.799	13.130	-12.098	1.00	28.13
ATOM	906	N	TYR	138	14.227	9.575	-8.250	1.00	18.00
ATOM	907	CA	TYR	138	13.340	8.793	-7.405	1.00	15.91
ATOM	908	C	TYR	138	13.736	8.609	-5.950	1.00	19.32
ATOM	909	O	TYR	138	13.063	7.879	-5.225	1.00	16.98
ATOM	910	CB	TYR	138	13.045	7.441	-8.052	1.00	16.71
ATOM	911	CG	TYR	138	12.114	7.486	-9.256	1.00	19.54
ATOM	912	CD1	TYR	138	12.488	8.115	-10.449	1.00	23.32
ATOM	913	CD2	TYR	138	10.863	6.872	-9.213	1.00	19.58
ATOM	914	CE1	TYR	138	11.631	8.130	-11.564	1.00	24.91
ATOM	915	CE2	TYR	138	10.003	6.883	-10.324	1.00	20.03
ATOM	916	CZ	TYR	138	10.396	7.507	-11.489	1.00	26.66
ATOM	917	OH	TYR	138	9.550	7.528	-12.570	1.00	26.09
ATOM	918	N	HIS	139	14.787	9.305	-5.507	1.00	17.01
ATOM	919	CA	HIS	139	15.305	9.227	-4.109	1.00	17.20
ATOM	920	C	HIS	139	15.303	7.828	-3.508	1.00	23.60
ATOM	921	O	HIS	139	14.920	7.649	-2.347	1.00	24.51
ATOM	922	CB	HIS	139	14.544	10.133	-3.130	1.00	18.62
ATOM	923	CG	HIS	139	14.222	11.495	-3.664	1.00	23.41
ATOM	924	ND1	HIS	139	15.148	12.292	-4.311	1.00	26.42
ATOM	925	CD2	HIS	139	13.067	12.198	-3.645	1.00	25.96
ATOM	926	CE1	HIS	139	14.574	13.430	-4.666	1.00	26.28
ATOM	927	NE2	HIS	139	13.308	13.397	-4.271	1.00	26.45
ATOM	928	N	SER	140	15.696	6.842	-4.305	1.00	22.35
ATOM	929	CA	SER	140	15.753	5.455	-3.852	1.00	22.86
ATOM	930	C	SER	140	17.193	5.111	-3.535	1.00	25.96
ATOM	931	O	SER	140	18.123	5.586	-4.187	1.00	26.58
ATOM	932	CB	SER	140	15.225	4.514	-4.933	1.00	27.27
ATOM	933	OG	SER	140	15.283	3.165	-4.519	1.00	35.77
ATOM	934	N	GLU	141	17.374	4.288	-2.520	1.00	21.11
ATOM	935	CA	GLU	141	18.704	3.893	-2.138	1.00	20.00
ATOM	936	C	GLU	141	19.142	2.726	-3.038	1.00	26.62
ATOM	937	O	GLU	141	18.301	1.967	-3.531	1.00	29.01
ATOM	938	CB	GLU	141	18.735	3.551	-0.642	1.00	21.07
ATOM	939	CG	GLU	141	17.921	4.524	0.228	1.00	33.28

ATOM	940	CD	GLU	141	18.578	4.855	1.554	1.00	69.28
ATOM	941	OE1	GLU	141	19.410	4.062	2.035	1.00	62.46
ATOM	942	OE2	GLU	141	18.252	5.920	2.118	1.00	84.87
ATOM	943	N	ALA	142	20.418	2.736	-3.418	1.00	21.23
ATOM	944	CA	ALA	142	21.024	1.684	-4.239	1.00	19.58
ATOM	945	C	ALA	142	22.395	1.431	-3.643	1.00	25.53
ATOM	946	O	ALA	142	23.119	2.372	-3.296	1.00	27.92
ATOM	947	CB	ALA	142	21.149	2.117	-5.696	1.00	19.69
ATOM	948	N	PHE	143	22.753	0.162	-3.521	1.00	19.73
ATOM	949	CA	PHE	143	24.026	-0.213	-2.914	1.00	17.41
ATOM	950	C	PHE	143	24.629	-1.343	-3.709	1.00	24.43
ATOM	951	O	PHE	143	23.927	-2.029	-4.445	1.00	26.35
ATOM	952	CB	PHE	143	23.799	-0.748	-1.494	1.00	17.55
ATOM	953	CG	PHE	143	22.861	0.076	-0.664	1.00	18.42
ATOM	954	CD1	PHE	143	23.343	1.113	0.126	1.00	20.30
ATOM	955	CD2	PHE	143	21.498	-0.198	-0.649	1.00	22.70
ATOM	956	CE1	PHE	143	22.490	1.864	0.926	1.00	23.21
ATOM	957	CE2	PHE	143	20.627	0.551	0.151	1.00	24.05
ATOM	958	CZ	PHE	143	21.130	1.585	0.939	1.00	22.11
ATOM	959	N	THR	144	25.924	-1.555	-3.543	1.00	20.15
ATOM	960	CA	THR	144	26.595	-2.654	-4.215	1.00	19.72
ATOM	961	C	THR	144	27.047	-3.575	-3.088	1.00	24.16
ATOM	962	O	THR	144	27.576	-3.102	-2.081	1.00	26.93
ATOM	963	CB	THR	144	27.798	-2.159	-5.049	1.00	26.86
ATOM	964	OG1	THR	144	28.633	-1.322	-4.242	1.00	28.49
ATOM	965	CG2	THR	144	27.324	-1.353	-6.228	1.00	29.29
ATOM	966	N	VAL	145	26.726	-4.857	-3.178	1.00	17.10
ATOM	967	CA	VAL	145	27.142	-5.787	-2.134	1.00	16.68
ATOM	968	C	VAL	145	27.894	-6.958	-2.735	1.00	24.06
ATOM	969	O	VAL	145	28.039	-7.051	-3.957	1.00	26.50
ATOM	970	CB	VAL	145	25.944	-6.307	-1.296	1.00	20.66
ATOM	971	CG1	VAL	145	25.320	-5.161	-0.516	1.00	21.22
ATOM	972	CG2	VAL	145	24.915	-6.973	-2.175	1.00	19.97
ATOM	973	N	ASN	146	28.439	-7.817	-1.882	1.00	19.01
ATOM	974	CA	ASN	146	29.158	-8.981	-2.374	1.00	17.59
ATOM	975	C	ASN	146	28.185	-10.130	-2.342	1.00	20.14
ATOM	976	O	ASN	146	27.917	-10.694	-1.282	1.00	20.83
ATOM	977	CB	ASN	146	30.368	-9.305	-1.497	1.00	19.20
ATOM	978	CG	ASN	146	31.056	-10.590	-1.906	1.00	31.52
ATOM	979	OD1	ASN	146	30.844	-11.106	-3.005	1.00	32.16
ATOM	980	ND2	ASN	146	31.855	-11.134	-1.007	1.00	23.72
ATOM	981	N	PHE	147	27.647	-10.476	-3.503	1.00	16.06
ATOM	982	CA	PHE	147	26.698	-11.574	-3.564	1.00	16.26
ATOM	983	C	PHE	147	27.387	-12.918	-3.518	1.00	23.42
ATOM	984	O	PHE	147	26.743	-13.954	-3.654	1.00	26.61
ATOM	985	CB	PHE	147	25.797	-11.471	-4.791	1.00	17.81
ATOM	986	CG	PHE	147	24.753	-10.406	-4.684	1.00	18.52
ATOM	987	CD1	PHE	147	23.615	-10.612	-3.912	1.00	20.66
ATOM	988	CD2	PHE	147	24.891	-9.206	-5.371	1.00	19.12
ATOM	989	CE1	PHE	147	22.621	-9.639	-3.836	1.00	20.73
ATOM	990	CE2	PHE	147	23.909	-8.237	-5.300	1.00	21.58
ATOM	991	CZ	PHE	147	22.772	-8.453	-4.532	1.00	19.82
ATOM	992	N	GLY	148	28.703	-12.895	-3.349	1.00	17.70
ATOM	993	CA	GLY	148	29.453	-14.132	-3.241	1.00	17.66

ATOM	994	C	GLY	148	29.147	-14.747	-1.884	1.00 23.36
ATOM	995	O	GLY	148	29.266	-15.959	-1.702	1.00 23.54
ATOM	996	N	ASP	149	28.835	-13.887	-0.912	1.00 20.63
ATOM	997	CA	ASP	149	28.469	-14.333	0.426	1.00 20.33
ATOM	998	C	ASP	149	26.958	-14.134	0.578	1.00 25.66
ATOM	999	O	ASP	149	26.498	-13.190	1.232	1.00 26.52
ATOM	1000	CB	ASP	149	29.220	-13.538	1.496	1.00 21.02
ATOM	1001	CG	ASP	149	29.092	-14.150	2.880	1.00 20.27
ATOM	1002	OD1	ASP	149	28.363	-15.132	3.086	1.00 19.33
ATOM	1003	OD2	ASP	149	29.750	-13.624	3.791	1.00 25.46
ATOM	1004	N	THR	150	26.205	-15.062	0.001	1.00 20.32
ATOM	1005	CA	THR	150	24.747	-15.040	0.013	1.00 18.86
ATOM	1006	C	THR	150	24.105	-14.621	1.338	1.00 21.45
ATOM	1007	O	THR	150	23.200	-13.784	1.363	1.00 20.49
ATOM	1008	CB	THR	150	24.195	-16.417	-0.405	1.00 24.26
ATOM	1009	OG1	THR	150	24.591	-16.690	-1.752	1.00 32.55
ATOM	1010	CG2	THR	150	22.684	-16.457	-0.293	1.00 19.05
ATOM	1011	N	GLU	151	24.601	-15.181	2.436	1.00 18.54
ATOM	1012	CA	GLU	151	24.082	-14.897	3.773	1.00 18.69
ATOM	1013	C	GLU	151	24.347	-13.469	4.195	1.00 22.02
ATOM	1014	O	GLU	151	23.470	-12.821	4.757	1.00 21.78
ATOM	1015	CB	GLU	151	24.692	-15.857	4.797	1.00 20.69
ATOM	1016	CG	GLU	151	23.943	-17.179	4.947	1.00 32.68
ATOM	1017	CD	GLU	151	22.941	-17.153	6.089	1.00 52.10
ATOM	1018	OE1	GLU	151	21.810	-16.675	5.911	1.00 56.21
ATOM	1019	OE2	GLU	151	23.309	-17.631	7.187	1.00 41.59
ATOM	1020	N	GLU	152	25.568	-13.001	3.940	1.00 17.95
ATOM	1021	CA	GLU	152	25.977	-11.642	4.274	1.00 17.12
ATOM	1022	C	GLU	152	25.135	-10.625	3.536	1.00 22.64
ATOM	1023	O	GLU	152	24.758	-9.602	4.104	1.00 22.21
ATOM	1024	CB	GLU	152	27.461	-11.430	3.958	1.00 17.92
ATOM	1025	CG	GLU	152	28.005	-10.055	4.315	1.00 15.21
ATOM	1026	CD	GLU	152	27.855	-9.711	5.778	1.00 19.13
ATOM	1027	OE1	GLU	152	27.469	-10.580	6.595	1.00 11.56
ATOM	1028	OE2	GLU	152	28.127	-8.546	6.116	1.00 14.61
ATOM	1029	N	ALA	153	24.767	-10.957	2.306	1.00 19.83
ATOM	1030	CA	ALA	153	23.931	-10.079	1.508	1.00 19.28
ATOM	1031	C	ALA	153	22.571	-9.958	2.188	1.00 22.30
ATOM	1032	O	ALA	153	22.112	-8.843	2.431	1.00 23.71
ATOM	1033	CB	ALA	153	23.798	-10.601	0.066	1.00 19.78
ATOM	1034	N	LYS	154	21.980	-11.084	2.588	1.00 16.20
ATOM	1035	CA	LYS	154	20.677	-11.029	3.255	1.00 16.61
ATOM	1036	C	LYS	154	20.759	-10.122	4.475	1.00 24.53
ATOM	1037	O	LYS	154	19.916	-9.247	4.655	1.00 25.74
ATOM	1038	CB	LYS	154	20.212	-12.391	3.754	1.00 19.25
ATOM	1039	CG	LYS	154	19.848	-13.422	2.730	1.00 18.46
ATOM	1040	CD	LYS	154	19.395	-14.664	3.474	1.00 21.03
ATOM	1041	CE	LYS	154	19.798	-15.955	2.776	1.00 29.51
ATOM	1042	NZ	LYS	154	19.175	-17.133	3.456	1.00 41.79
ATOM	1043	N	LYS	155	21.741	-10.364	5.342	1.00 21.41
ATOM	1044	CA	LYS	155	21.890	-9.542	6.531	1.00 21.15
ATOM	1045	C	LYS	155	22.018	-8.088	6.094	1.00 26.11
ATOM	1046	O	LYS	155	21.184	-7.253	6.444	1.00 27.67
ATOM	1047	CB	LYS	155	23.102	-9.974	7.369	1.00 22.36

ATOM	1048	CG	LYS	155	23.154	-9.290	8.732	1.00	45.02
ATOM	1049	CD	LYS	155	24.283	-9.774	9.598	1.00	62.54
ATOM	1050	CE	LYS	155	24.327	-8.992	10.905	1.00	92.82
ATOM	1051	NZ	LYS	155	25.397	-9.487	11.812	1.00	110.00
ATOM	1052	N	GLN	156	22.975	-7.847	5.212	1.00	19.93
ATOM	1053	CA	GLN	156	23.264	-6.521	4.679	1.00	19.33
ATOM	1054	C	GLN	156	22.015	-5.809	4.166	1.00	22.80
ATOM	1055	O	GLN	156	21.831	-4.601	4.363	1.00	23.72
ATOM	1056	CB	GLN	156	24.278	-6.652	3.543	1.00	21.20
ATOM	1057	CG	GLN	156	25.363	-5.589	3.538	1.00	57.09
ATOM	1058	CD	GLN	156	26.548	-5.987	2.678	1.00	93.87
ATOM	1059	OE1	GLN	156	26.866	-7.171	2.529	1.00	94.48
ATOM	1060	NE2	GLN	156	27.216	-4.999	2.115	1.00	89.29
ATOM	1061	N	ILE	157	21.142	-6.585	3.543	1.00	17.92
ATOM	1062	CA	ILE	157	19.899	-6.082	2.970	1.00	18.11
ATOM	1063	C	ILE	157	18.868	-5.832	4.062	1.00	25.86
ATOM	1064	O	ILE	157	18.338	-4.723	4.203	1.00	27.68
ATOM	1065	CB	ILE	157	19.330	-7.108	1.970	1.00	21.30
ATOM	1066	CG1	ILE	157	20.209	-7.151	0.716	1.00	21.24
ATOM	1067	CG2	ILE	157	17.871	-6.825	1.672	1.00	21.77
ATOM	1068	CD1	ILE	157	19.683	-8.024	-0.396	1.00	29.59
ATOM	1069	N	ASN	158	18.578	-6.895	4.804	1.00	20.59
ATOM	1070	CA	ASN	158	17.632	-6.879	5.901	1.00	19.17
ATOM	1071	C	ASN	158	17.949	-5.804	6.941	1.00	23.91
ATOM	1072	O	ASN	158	17.049	-5.178	7.498	1.00	25.85
ATOM	1073	CB	ASN	158	17.542	-8.284	6.492	1.00	15.15
ATOM	1074	CG	ASN	158	16.834	-9.240	5.549	1.00	28.18
ATOM	1075	OD1	ASN	158	15.934	-8.832	4.806	1.00	35.81
ATOM	1076	ND2	ASN	158	17.214	-10.506	5.577	1.00	16.31
ATOM	1077	N	ASP	159	19.230	-5.511	7.097	1.00	17.77
ATOM	1078	CA	ASP	159	19.682	-4.481	8.020	1.00	16.35
ATOM	1079	C	ASP	159	19.163	-3.153	7.484	1.00	23.88
ATOM	1080	O	ASP	159	18.614	-2.361	8.230	1.00	25.41
ATOM	1081	CB	ASP	159	21.204	-4.418	8.066	1.00	17.14
ATOM	1082	CG	ASP	159	21.817	-5.525	8.903	1.00	24.66
ATOM	1083	OD1	ASP	159	21.088	-6.358	9.471	1.00	21.78
ATOM	1084	OD2	ASP	159	23.068	-5.554	8.994	1.00	34.61
ATOM	1085	N	TYR	160	19.309	-2.929	6.178	1.00	18.74
ATOM	1086	CA	TYR	160	18.845	-1.697	5.546	1.00	17.14
ATOM	1087	C	TYR	160	17.381	-1.434	5.876	1.00	21.00
ATOM	1088	O	TYR	160	17.038	-0.379	6.410	1.00	20.20
ATOM	1089	CB	TYR	160	19.051	-1.791	4.034	1.00	17.42
ATOM	1090	CG	TYR	160	18.250	-0.818	3.205	1.00	18.83
ATOM	1091	CD1	TYR	160	18.551	0.541	3.195	1.00	21.81
ATOM	1092	CD2	TYR	160	17.190	-1.261	2.416	1.00	19.83
ATOM	1093	CE1	TYR	160	17.815	1.432	2.420	1.00	24.46
ATOM	1094	CE2	TYR	160	16.449	-0.372	1.638	1.00	20.73
ATOM	1095	CZ	TYR	160	16.770	0.970	1.642	1.00	30.99
ATOM	1096	OH	TYR	160	16.064	1.847	0.853	1.00	40.24
ATOM	1097	N	VAL	161	16.537	-2.417	5.595	1.00	16.86
ATOM	1098	CA	VAL	161	15.113	-2.316	5.850	1.00	16.19
ATOM	1099	C	VAL	161	14.841	-2.067	7.326	1.00	20.13
ATOM	1100	O	VAL	161	14.189	-1.090	7.677	1.00	20.42
ATOM	1101	CB	VAL	161	14.392	-3.605	5.426	1.00	20.73

ATOM	1102	CG1	VAL	161	12.892	-3.492	5.677	1.00	19.90
ATOM	1103	CG2	VAL	161	14.667	-3.898	3.973	1.00	20.69
ATOM	1104	N	GLU	162	15.371	-2.934	8.182	1.00	16.21
ATOM	1105	CA	GLU	162	15.172	-2.822	9.623	1.00	15.88
ATOM	1106	C	GLU	162	15.533	-1.423	10.102	1.00	22.69
ATOM	1107	O	GLU	162	14.710	-0.736	10.705	1.00	23.11
ATOM	1108	CB	GLU	162	16.013	-3.866	10.338	1.00	17.15
ATOM	1109	CG	GLU	162	15.809	-3.942	11.835	1.00	30.05
ATOM	1110	CD	GLU	162	16.585	-5.079	12.467	1.00	54.95
ATOM	1111	OE1	GLU	162	16.758	-6.127	11.809	1.00	58.16
ATOM	1112	OE2	GLU	162	17.005	-4.924	13.633	1.00	54.90
ATOM	1113	N	LYS	163	16.757	-1.009	9.800	1.00	19.73
ATOM	1114	CA	LYS	163	17.286	0.304	10.145	1.00	19.34
ATOM	1115	C	LYS	163	16.342	1.386	9.625	1.00	22.08
ATOM	1116	O	LYS	163	16.012	2.337	10.332	1.00	22.56
ATOM	1117	CB	LYS	163	18.685	0.441	9.517	1.00	23.21
ATOM	1118	CG	LYS	163	19.222	1.855	9.274	1.00	52.18
ATOM	1119	CD	LYS	163	20.483	1.803	8.401	1.00	69.36
ATOM	1120	CE	LYS	163	21.113	3.174	8.140	1.00	79.02
ATOM	1121	NZ	LYS	163	22.310	3.063	7.249	1.00	90.37
ATOM	1122	N	GLY	164	15.831	1.159	8.422	1.00	18.15
ATOM	1123	CA	GLY	164	14.939	2.107	7.785	1.00	18.81
ATOM	1124	C	GLY	164	13.534	2.111	8.346	1.00	25.15
ATOM	1125	O	GLY	164	12.854	3.127	8.272	1.00	27.19
ATOM	1126	N	THR	165	13.102	0.985	8.910	1.00	19.62
ATOM	1127	CA	THR	165	11.766	0.861	9.492	1.00	18.76
ATOM	1128	C	THR	165	11.944	0.902	11.005	1.00	26.62
ATOM	1129	O	THR	165	11.008	0.645	11.774	1.00	27.29
ATOM	1130	CB	THR	165	11.081	-0.484	9.116	1.00	12.69
ATOM	1131	OG1	THR	165	11.893	-1.582	9.557	1.00	15.15
ATOM	1132	CG2	THR	165	10.842	-0.585	7.611	1.00	3.04
ATOM	1133	N	GLN	166	13.172	1.211	11.409	1.00	23.31
ATOM	1134	CA	GLN	166	13.570	1.276	12.808	1.00	22.33
ATOM	1135	C	GLN	166	13.075	0.102	13.664	1.00	27.93
ATOM	1136	O	GLN	166	12.495	0.276	14.752	1.00	29.62
ATOM	1137	CB	GLN	166	13.278	2.656	13.417	1.00	23.16
ATOM	1138	CG	GLN	166	14.291	3.701	12.952	1.00	54.02
ATOM	1139	CD	GLN	166	14.384	4.920	13.852	1.00	89.44
ATOM	1140	OE1	GLN	166	13.958	4.907	15.011	1.00	87.60
ATOM	1141	NE2	GLN	166	14.968	5.984	13.322	1.00	86.30
ATOM	1142	N	GLY	167	13.350	-1.101	13.159	1.00	19.76
ATOM	1143	CA	GLY	167	12.995	-2.305	13.872	1.00	17.73
ATOM	1144	C	GLY	167	11.645	-2.906	13.598	1.00	18.99
ATOM	1145	O	GLY	167	11.356	-3.969	14.127	1.00	17.55
ATOM	1146	N	LYS	168	10.814	-2.257	12.791	1.00	18.38
ATOM	1147	CA	LYS	168	9.497	-2.822	12.507	1.00	20.25
ATOM	1148	C	LYS	168	9.595	-4.015	11.567	1.00	27.25
ATOM	1149	O	LYS	168	8.819	-4.970	11.667	1.00	30.06
ATOM	1150	CB	LYS	168	8.529	-1.784	11.941	1.00	22.56
ATOM	1151	CG	LYS	168	7.071	-2.206	12.103	1.00	39.22
ATOM	1152	CD	LYS	168	6.708	-2.323	13.588	1.00	58.14
ATOM	1153	CE	LYS	168	5.315	-2.908	13.833	1.00	64.40
ATOM	1154	NZ	LYS	168	5.186	-4.343	13.430	1.00	71.27
ATOM	1155	N	ILE	169	10.517	-3.935	10.618	1.00	21.26

ATOM	1156	CA	ILE	169	10.716	-5.031	9.682	1.00	19.37
ATOM	1157	C	ILE	169	12.096	-5.644	9.941	1.00	23.05
ATOM	1158	O	ILE	169	13.127	-4.966	9.921	1.00	24.91
ATOM	1159	CB	ILE	169	10.525	-4.573	8.210	1.00	21.73
ATOM	1160	CG1	ILE	169	9.060	-4.139	7.984	1.00	22.05
ATOM	1161	CG2	ILE	169	10.910	-5.699	7.258	1.00	20.93
ATOM	1162	CD1	ILE	169	8.782	-3.495	6.634	1.00	17.20
ATOM	1163	N	VAL	170	12.096	-6.930	10.242	1.00	16.49
ATOM	1164	CA	VAL	170	13.321	-7.637	10.546	1.00	15.72
ATOM	1165	C	VAL	170	13.470	-8.824	9.597	1.00	19.76
ATOM	1166	O	VAL	170	12.478	-9.461	9.237	1.00	17.77
ATOM	1167	CB	VAL	170	13.279	-8.079	11.998	1.00	20.38
ATOM	1168	CG1	VAL	170	13.353	-6.848	12.905	1.00	19.80
ATOM	1169	CG2	VAL	170	11.979	-8.823	12.259	1.00	21.00
ATOM	1170	N	ASP	171	14.694	-9.035	9.114	1.00	19.34
ATOM	1171	CA	ASP	171	15.021	-10.112	8.162	1.00	20.38
ATOM	1172	C	ASP	171	13.923	-10.430	7.144	1.00	22.67
ATOM	1173	O	ASP	171	13.271	-11.473	7.179	1.00	23.02
ATOM	1174	CB	ASP	171	15.675	-11.359	8.832	1.00	23.70
ATOM	1175	CG	ASP	171	14.674	-12.312	9.480	1.00	42.06
ATOM	1176	OD1	ASP	171	13.524	-11.929	9.772	1.00	48.32
ATOM	1177	OD2	ASP	171	15.067	-13.473	9.715	1.00	45.87
ATOM	1178	N	LEU	172	13.731	-9.474	6.241	1.00	18.15
ATOM	1179	CA	LEU	172	12.723	-9.547	5.196	1.00	17.36
ATOM	1180	C	LEU	172	12.976	-10.702	4.250	1.00	24.59
ATOM	1181	O	LEU	172	12.062	-11.465	3.915	1.00	26.72
ATOM	1182	CB	LEU	172	12.715	-8.238	4.413	1.00	16.47
ATOM	1183	CG	LEU	172	11.669	-8.014	3.338	1.00	20.87
ATOM	1184	CD1	LEU	172	10.307	-8.399	3.853	1.00	20.88
ATOM	1185	CD2	LEU	172	11.704	-6.568	2.908	1.00	21.64
ATOM	1186	N	VAL	173	14.227	-10.804	3.812	1.00	19.02
ATOM	1187	CA	VAL	173	14.662	-11.837	2.892	1.00	16.81
ATOM	1188	C	VAL	173	15.137	-13.031	3.701	1.00	20.99
ATOM	1189	O	VAL	173	16.010	-12.901	4.555	1.00	22.14
ATOM	1190	CB	VAL	173	15.784	-11.312	1.970	1.00	19.26
ATOM	1191	CG1	VAL	173	16.266	-12.402	1.023	1.00	19.04
ATOM	1192	CG2	VAL	173	15.285	-10.109	1.190	1.00	18.18
ATOM	1193	N	LYS	174	14.521	-14.179	3.441	1.00	17.06
ATOM	1194	CA	LYS	174	14.828	-15.430	4.118	1.00	17.44
ATOM	1195	C	LYS	174	15.835	-16.268	3.331	1.00	25.16
ATOM	1196	O	LYS	174	16.335	-17.274	3.841	1.00	27.74
ATOM	1197	CB	LYS	174	13.536	-16.227	4.316	1.00	20.15
ATOM	1198	CG	LYS	174	12.400	-15.414	4.914	1.00	35.14
ATOM	1199	CD	LYS	174	12.437	-15.391	6.423	1.00	47.19
ATOM	1200	CE	LYS	174	11.459	-14.373	6.961	1.00	58.72
ATOM	1201	NZ	LYS	174	10.822	-14.807	8.225	1.00	76.00
ATOM	1202	N	GLU	175	16.075	-15.900	2.074	1.00	19.67
ATOM	1203	CA	GLU	175	17.034	-16.614	1.229	1.00	19.84
ATOM	1204	C	GLU	175	17.217	-16.011	-0.162	1.00	26.26
ATOM	1205	O	GLU	175	16.314	-15.359	-0.678	1.00	27.25
ATOM	1206	CB	GLU	175	16.710	-18.111	1.131	1.00	21.25
ATOM	1207	CG	GLU	175	15.298	-18.481	0.674	1.00	38.11
ATOM	1208	CD	GLU	175	15.033	-19.975	0.813	1.00	78.80
ATOM	1209	OE1	GLU	175	15.785	-20.646	1.555	1.00	83.96

ATOM	1210	OE2	GLU	175	14.066	-20.476	0.199	1.00	82.02
ATOM	1211	N	LEU	176	18.398	-16.215	-0.749	1.00	20.61
ATOM	1212	CA	LEU	176	18.719	-15.688	-2.076	1.00	18.97
ATOM	1213	C	LEU	176	19.145	-16.786	-3.038	1.00	23.08
ATOM	1214	O	LEU	176	19.766	-17.779	-2.637	1.00	21.51
ATOM	1215	CB	LEU	176	19.851	-14.657	-2.005	1.00	19.21
ATOM	1216	CG	LEU	176	19.592	-13.270	-1.414	1.00	25.41
ATOM	1217	CD1	LEU	176	20.909	-12.527	-1.314	1.00	24.90
ATOM	1218	CD2	LEU	176	18.613	-12.504	-2.287	1.00	31.01
ATOM	1219	N	ASP	177	18.817	-16.595	-4.315	1.00	21.83
ATOM	1220	CA	ASP	177	19.174	-17.555	-5.370	1.00	21.94
ATOM	1221	C	ASP	177	20.675	-17.647	-5.524	1.00	28.47
ATOM	1222	O	ASP	177	21.414	-16.775	-5.070	1.00	31.66
ATOM	1223	CB	ASP	177	18.545	-17.182	-6.714	1.00	24.78
ATOM	1224	CG	ASP	177	17.025	-17.142	-6.655	1.00	50.17
ATOM	1225	OD1	ASP	177	16.363	-18.193	-6.746	1.00	51.41
ATOM	1226	OD2	ASP	177	16.483	-16.020	-6.513	1.00	63.80
ATOM	1227	N	ARG	178	21.103	-18.679	-6.236	1.00	22.85
ATOM	1228	CA	ARG	178	22.522	-18.958	-6.470	1.00	21.85
ATOM	1229	C	ARG	178	23.191	-17.927	-7.386	1.00	24.51
ATOM	1230	O	ARG	178	24.348	-17.569	-7.189	1.00	26.94
ATOM	1231	CB	ARG	178	22.686	-20.388	-7.036	1.00	24.68
ATOM	1232	CG	ARG	178	21.805	-21.462	-6.360	1.00	36.59
ATOM	1233	CD	ARG	178	20.349	-21.385	-6.826	1.00	61.75
ATOM	1234	NE	ARG	178	19.426	-22.048	-5.902	1.00	86.02
ATOM	1235	CZ	ARG	178	18.120	-21.795	-5.819	1.00	109.62
ATOM	1236	NH1	ARG	178	17.556	-20.877	-6.589	1.00	106.33
ATOM	1237	NH2	ARG	178	17.364	-22.485	-4.972	1.00	95.24
ATOM	1238	N	ASP	179	22.444	-17.422	-8.355	1.00	19.98
ATOM	1239	CA	ASP	179	22.946	-16.433	-9.310	1.00	20.64
ATOM	1240	C	ASP	179	22.460	-15.014	-8.999	1.00	26.46
ATOM	1241	O	ASP	179	22.314	-14.174	-9.896	1.00	27.73
ATOM	1242	CB	ASP	179	22.532	-16.813	-10.737	1.00	24.57
ATOM	1243	CG	ASP	179	21.033	-17.092	-10.856	1.00	59.63
ATOM	1244	OD1	ASP	179	20.259	-16.796	-9.918	1.00	65.53
ATOM	1245	OD2	ASP	179	20.639	-17.624	-11.919	1.00	71.83
ATOM	1246	N	THR	180	22.233	-14.739	-7.729	1.00	21.49
ATOM	1247	CA	THR	180	21.760	-13.426	-7.364	1.00	20.37
ATOM	1248	C	THR	180	22.871	-12.388	-7.545	1.00	23.03
ATOM	1249	O	THR	180	23.967	-12.536	-6.998	1.00	22.71
ATOM	1250	CB	THR	180	21.225	-13.396	-5.915	1.00	32.99
ATOM	1251	OG1	THR	180	20.180	-14.370	-5.763	1.00	31.89
ATOM	1252	CG2	THR	180	20.663	-12.024	-5.589	1.00	34.35
ATOM	1253	N	VAL	181	22.607	-11.385	-8.383	1.00	18.85
ATOM	1254	CA	VAL	181	23.554	-10.297	-8.634	1.00	18.00
ATOM	1255	C	VAL	181	22.866	-8.934	-8.541	1.00	21.23
ATOM	1256	O	VAL	181	23.540	-7.901	-8.499	1.00	22.38
ATOM	1257	CB	VAL	181	24.245	-10.404	-10.022	1.00	21.67
ATOM	1258	CG1	VAL	181	25.156	-11.615	-10.072	1.00	21.73
ATOM	1259	CG2	VAL	181	23.209	-10.447	-11.136	1.00	21.58
ATOM	1260	N	PHE	182	21.537	-8.943	-8.454	1.00	15.29
ATOM	1261	CA	PHE	182	20.732	-7.723	-8.378	1.00	14.49
ATOM	1262	C	PHE	182	19.496	-8.014	-7.527	1.00	20.22
ATOM	1263	O	PHE	182	18.733	-8.929	-7.838	1.00	20.58

ATOM	1264	CB	PHE	182	20.337	-7.315	-9.803	1.00	16.32
ATOM	1265	CG	PHE	182	19.567	-6.019	-9.904	1.00	17.71
ATOM	1266	CD1	PHE	182	19.511	-5.118	-8.845	1.00	21.27
ATOM	1267	CD2	PHE	182	18.926	-5.682	-11.093	1.00	18.66
ATOM	1268	CE1	PHE	182	18.802	-3.913	-8.962	1.00	21.29
ATOM	1269	CE2	PHE	182	18.219	-4.485	-11.214	1.00	20.48
ATOM	1270	CZ	PHE	182	18.167	-3.598	-10.154	1.00	18.22
ATOM	1271	N	ALA	183	19.343	-7.281	-6.424	1.00	18.30
ATOM	1272	CA	ALA	183	18.203	-7.455	-5.501	1.00	17.95
ATOM	1273	C	ALA	183	17.461	-6.156	-5.205	1.00	19.05
ATOM	1274	O	ALA	183	18.074	-5.114	-4.981	1.00	17.29
ATOM	1275	CB	ALA	183	18.650	-8.104	-4.190	1.00	18.82
ATOM	1276	N	LEU	184	16.136	-6.246	-5.163	1.00	16.09
ATOM	1277	CA	LEU	184	15.266	-5.095	-4.919	1.00	16.36
ATOM	1278	C	LEU	184	14.435	-5.339	-3.673	1.00	17.70
ATOM	1279	O	LEU	184	13.743	-6.354	-3.560	1.00	17.17
ATOM	1280	CB	LEU	184	14.334	-4.850	-6.132	1.00	16.99
ATOM	1281	CG	LEU	184	13.436	-3.594	-6.213	1.00	22.65
ATOM	1282	CD1	LEU	184	12.979	-3.361	-7.627	1.00	21.80
ATOM	1283	CD2	LEU	184	12.228	-3.692	-5.287	1.00	28.05
ATOM	1284	N	VAL	185	14.492	-4.403	-2.742	1.00	14.81
ATOM	1285	CA	VAL	185	13.721	-4.520	-1.515	1.00	16.22
ATOM	1286	C	VAL	185	12.849	-3.270	-1.363	1.00	18.85
ATOM	1287	O	VAL	185	13.344	-2.140	-1.295	1.00	16.95
ATOM	1288	CB	VAL	185	14.641	-4.767	-0.294	1.00	20.90
ATOM	1289	CG1	VAL	185	13.819	-4.876	0.971	1.00	21.00
ATOM	1290	CG2	VAL	185	15.433	-6.048	-0.496	1.00	20.06
ATOM	1291	N	ASN	186	11.541	-3.490	-1.382	1.00	16.14
ATOM	1292	CA	ASN	186	10.551	-2.427	-1.292	1.00	16.68
ATOM	1293	C	ASN	186	9.653	-2.671	-0.083	1.00	21.69
ATOM	1294	O	ASN	186	9.051	-3.733	0.052	1.00	23.15
ATOM	1295	CB	ASN	186	9.734	-2.398	-2.595	1.00	12.94
ATOM	1296	CG	ASN	186	8.838	-1.204	-2.696	1.00	19.95
ATOM	1297	OD1	ASN	186	7.664	-1.250	-2.325	1.00	11.91
ATOM	1298	ND2	ASN	186	9.391	-0.106	-3.179	1.00	10.24
ATOM	1299	N	TYR	187	9.578	-1.687	0.801	1.00	15.75
ATOM	1300	CA	TYR	187	8.773	-1.806	2.002	1.00	14.62
ATOM	1301	C	TYR	187	8.078	-0.471	2.290	1.00	22.42
ATOM	1302	O	TYR	187	8.484	0.581	1.772	1.00	23.11
ATOM	1303	CB	TYR	187	9.676	-2.184	3.176	1.00	15.24
ATOM	1304	CG	TYR	187	10.667	-1.084	3.550	1.00	18.84
ATOM	1305	CD1	TYR	187	10.268	0.007	4.335	1.00	21.93
ATOM	1306	CD2	TYR	187	12.004	-1.132	3.127	1.00	19.78
ATOM	1307	CE1	TYR	187	11.171	1.013	4.692	1.00	23.73
ATOM	1308	CE2	TYR	187	12.911	-0.128	3.483	1.00	20.67
ATOM	1309	CZ	TYR	187	12.484	0.935	4.266	1.00	28.94
ATOM	1310	OH	TYR	187	13.374	1.906	4.658	1.00	29.27
ATOM	1311	N	ILE	188	7.058	-0.517	3.144	1.00	19.02
ATOM	1312	CA	ILE	188	6.304	0.673	3.531	1.00	18.03
ATOM	1313	C	ILE	188	5.626	0.411	4.853	1.00	23.51
ATOM	1314	O	ILE	188	4.922	-0.581	5.003	1.00	25.66
ATOM	1315	CB	ILE	188	5.238	1.063	2.484	1.00	19.71
ATOM	1316	CG1	ILE	188	4.464	2.302	2.940	1.00	19.85
ATOM	1317	CG2	ILE	188	4.308	-0.091	2.233	1.00	16.85

ATOM	1318	CD1	ILE	188	3.574	2.900	1.869	1.00	28.04
ATOM	1319	N	PHE	189	5.910	1.256	5.833	1.00	18.63
ATOM	1320	CA	PHE	189	5.309	1.119	7.145	1.00	17.30
ATOM	1321	C	PHE	189	4.489	2.368	7.452	1.00	18.72
ATOM	1322	O	PHE	189	5.002	3.490	7.368	1.00	16.24
ATOM	1323	CB	PHE	189	6.383	0.922	8.217	1.00	19.37
ATOM	1324	CG	PHE	189	5.850	1.018	9.616	1.00	21.45
ATOM	1325	CD1	PHE	189	5.200	-0.063	10.199	1.00	23.96
ATOM	1326	CD2	PHE	189	5.930	2.213	10.327	1.00	23.47
ATOM	1327	CE1	PHE	189	4.637	0.048	11.459	1.00	24.52
ATOM	1328	CE2	PHE	189	5.366	2.319	11.586	1.00	25.92
ATOM	1329	CZ	PHE	189	4.719	1.237	12.149	1.00	23.37
ATOM	1330	N	PHE	190	3.222	2.168	7.807	1.00	15.59
ATOM	1331	CA	PHE	190	2.340	3.275	8.123	1.00	15.41
ATOM	1332	C	PHE	190	1.589	3.073	9.425	1.00	21.53
ATOM	1333	O	PHE	190	1.228	1.957	9.784	1.00	22.76
ATOM	1334	CB	PHE	190	1.335	3.500	7.002	1.00	17.31
ATOM	1335	CG	PHE	190	0.448	4.690	7.222	1.00	18.57
ATOM	1336	CD1	PHE	190	0.996	5.967	7.286	1.00	21.44
ATOM	1337	CD2	PHE	190	-0.927	4.543	7.384	1.00	19.70
ATOM	1338	CE1	PHE	190	0.193	7.067	7.504	1.00	22.32
ATOM	1339	CE2	PHE	190	-1.733	5.647	7.602	1.00	22.76
ATOM	1340	CZ	PHE	190	-1.177	6.904	7.662	1.00	21.21
ATOM	1341	N	LYS	191	1.369	4.171	10.130	1.00	19.61
ATOM	1342	CA	LYS	191	0.640	4.168	11.386	1.00	20.03
ATOM	1343	C	LYS	191	0.261	5.617	11.631	1.00	23.60
ATOM	1344	O	LYS	191	0.952	6.344	12.344	1.00	24.22
ATOM	1345	CB	LYS	191	1.514	3.650	12.525	1.00	24.39
ATOM	1346	CG	LYS	191	0.776	3.575	13.844	1.00	51.75
ATOM	1347	CD	LYS	191	1.726	3.537	15.032	1.00	59.10
ATOM	1348	CE	LYS	191	0.934	3.604	16.307	1.00	60.54
ATOM	1349	NZ	LYS	191	0.090	4.820	16.277	1.00	61.59
ATOM	1350	N	GLY	192	-0.751	6.065	10.899	1.00	18.83
ATOM	1351	CA	GLY	192	-1.207	7.431	11.028	1.00	17.89
ATOM	1352	C	GLY	192	-2.017	7.706	12.270	1.00	21.28
ATOM	1353	O	GLY	192	-2.533	6.800	12.925	1.00	21.21
ATOM	1354	N	LYS	193	-2.085	8.980	12.620	1.00	18.93
ATOM	1355	CA	LYS	193	-2.840	9.414	13.779	1.00	20.11
ATOM	1356	C	LYS	193	-4.170	9.929	13.239	1.00	28.57
ATOM	1357	O	LYS	193	-4.200	10.621	12.222	1.00	30.68
ATOM	1358	CB	LYS	193	-2.066	10.518	14.492	1.00	22.77
ATOM	1359	CG	LYS	193	-0.605	10.152	14.635	1.00	59.22
ATOM	1360	CD	LYS	193	0.255	11.289	15.098	1.00	85.61
ATOM	1361	CE	LYS	193	1.716	10.864	15.104	1.00	104.77
ATOM	1362	NZ	LYS	193	2.595	11.990	15.496	1.00	110.00
ATOM	1363	N	TRP	194	-5.275	9.502	13.842	1.00	22.28
ATOM	1364	CA	TRP	194	-6.580	9.956	13.389	1.00	19.23
ATOM	1365	C	TRP	194	-6.729	11.449	13.600	1.00	22.08
ATOM	1366	O	TRP	194	-6.345	11.975	14.642	1.00	20.61
ATOM	1367	CB	TRP	194	-7.709	9.232	14.127	1.00	16.80
ATOM	1368	CG	TRP	194	-7.820	7.791	13.793	1.00	17.43
ATOM	1369	CD1	TRP	194	-7.806	6.739	14.660	1.00	20.34
ATOM	1370	CD2	TRP	194	-7.894	7.235	12.478	1.00	17.41
ATOM	1371	NE1	TRP	194	-7.850	5.558	13.962	1.00	20.08

ATOM	1372	CE2	TRP	194	-7.920	5.832	12.633	1.00	21.75
ATOM	1373	CE3	TRP	194	-7.961	7.785	11.198	1.00	18.74
ATOM	1374	CZ2	TRP	194	-7.969	4.977	11.530	1.00	20.89
ATOM	1375	CZ3	TRP	194	-8.009	6.933	10.111	1.00	20.61
ATOM	1376	CH2	TRP	194	-8.028	5.542	10.286	1.00	21.45
ATOM	1377	N	GLU	195	-7.308	12.105	12.578	1.00	18.47
ATOM	1378	CA	GLU	195	-7.643	13.509	12.721	1.00	17.31
ATOM	1379	C	GLU	195	-8.716	13.627	13.767	1.00	24.91
ATOM	1380	O	GLU	195	-8.750	14.601	14.501	1.00	26.50
ATOM	1381	CB	GLU	195	-8.193	13.966	11.359	1.00	17.55
ATOM	1382	CG	GLU	195	-8.065	15.493	11.231	1.00	17.56
ATOM	1383	CD	GLU	195	-8.452	15.898	9.839	1.00	24.67
ATOM	1384	OE1	GLU	195	-9.680	15.929	9.553	1.00	8.00
ATOM	1385	OE2	GLU	195	-7.532	16.193	9.032	1.00	29.08
ATOM	1386	N	ARG	196	-9.582	12.597	13.838	1.00	20.95
ATOM	1387	CA	ARG	196	-10.576	12.563	14.894	1.00	19.29
ATOM	1388	C	ARG	196	-10.401	11.246	15.606	1.00	19.82
ATOM	1389	O	ARG	196	-10.955	10.248	15.172	1.00	17.50
ATOM	1390	CB	ARG	196	-11.967	12.693	14.247	1.00	17.74
ATOM	1391	CG	ARG	196	-12.101	14.095	13.626	1.00	28.49
ATOM	1392	CD	ARG	196	-13.389	14.170	12.788	1.00	44.06
ATOM	1393	NE	ARG	196	-13.398	15.427	12.063	1.00	68.61
ATOM	1394	CZ	ARG	196	-14.509	15.946	11.626	1.00	90.69
ATOM	1395	NH1	ARG	196	-15.650	15.352	11.819	1.00	78.16
ATOM	1396	NH2	ARG	196	-14.475	17.076	10.984	1.00	79.20
ATOM	1397	N	PRO	197	-9.608	11.228	16.701	1.00	16.16
ATOM	1398	CA	PRO	197	-9.262	9.981	17.351	1.00	14.33
ATOM	1399	C	PRO	197	-10.380	9.296	18.090	1.00	19.09
ATOM	1400	O	PRO	197	-11.441	9.847	18.328	1.00	19.66
ATOM	1401	CB	PRO	197	-8.165	10.412	18.347	1.00	16.11
ATOM	1402	CG	PRO	197	-8.160	11.956	18.384	1.00	22.80
ATOM	1403	CD	PRO	197	-9.018	12.450	17.203	1.00	18.02
ATOM	1404	N	PHE	198	-10.067	8.035	18.439	1.00	15.54
ATOM	1405	CA	PHE	198	-10.958	7.199	19.238	1.00	15.37
ATOM	1406	C	PHE	198	-10.378	7.325	20.641	1.00	25.44
ATOM	1407	O	PHE	198	-9.150	7.366	20.823	1.00	28.47
ATOM	1408	CB	PHE	198	-10.867	5.717	18.834	1.00	16.18
ATOM	1409	CG	PHE	198	-11.560	5.392	17.553	1.00	18.18
ATOM	1410	CD1	PHE	198	-12.931	5.214	17.519	1.00	22.32
ATOM	1411	CD2	PHE	198	-10.847	5.303	16.366	1.00	20.91
ATOM	1412	CE1	PHE	198	-13.589	4.958	16.321	1.00	23.71
ATOM	1413	CE2	PHE	198	-11.490	5.049	15.172	1.00	23.38
ATOM	1414	CZ	PHE	198	-12.866	4.877	15.146	1.00	21.79
ATOM	1415	N	GLU	199	-11.268	7.362	21.648	1.00	21.15
ATOM	1416	CA	GLU	199	-10.759	7.396	23.004	1.00	21.66
ATOM	1417	C	GLU	199	-10.458	6.001	23.469	1.00	25.73
ATOM	1418	O	GLU	199	-11.331	5.146	23.467	1.00	27.78
ATOM	1419	CB	GLU	199	-11.738	8.127	23.941	1.00	24.14
ATOM	1420	CG	GLU	199	-11.845	9.597	23.490	1.00	44.18
ATOM	1421	CD	GLU	199	-12.328	10.519	24.577	1.00	83.32
ATOM	1422	OE1	GLU	199	-12.652	10.035	25.695	1.00	77.92
ATOM	1423	OE2	GLU	199	-12.381	11.749	24.309	1.00	89.79
ATOM	1424	N	VAL	200	-9.187	5.793	23.862	1.00	18.99
ATOM	1425	CA	VAL	200	-8.765	4.484	24.356	1.00	17.54

ATOM	1426	C	VAL	200	-9.690	3.888	25.421	1.00	21.63
ATOM	1427	O	VAL	200	-9.879	2.676	25.477	1.00	22.09
ATOM	1428	CB	VAL	200	-7.319	4.539	24.927	1.00	21.35
ATOM	1429	CG1	VAL	200	-6.796	3.147	25.174	1.00	21.50
ATOM	1430	CG2	VAL	200	-6.395	5.278	23.981	1.00	21.61
ATOM	1431	N	LYS	201	-10.319	4.742	26.217	1.00	19.04
ATOM	1432	CA	LYS	201	-11.192	4.262	27.275	1.00	18.50
ATOM	1433	C	LYS	201	-12.267	3.344	26.726	1.00	26.40
ATOM	1434	O	LYS	201	-12.581	2.335	27.342	1.00	26.71
ATOM	1435	CB	LYS	201	-11.833	5.430	28.023	1.00	18.67
ATOM	1436	CG	LYS	201	-12.888	6.216	27.249	1.00	18.75
ATOM	1437	CD	LYS	201	-13.518	7.283	28.119	1.00	18.80
ATOM	1438	CE	LYS	201	-14.672	7.970	27.427	1.00	32.20
ATOM	1439	NZ	LYS	201	-15.326	8.972	28.307	1.00	45.27
ATOM	1440	N	ASP	202	-12.780	3.682	25.544	1.00	25.30
ATOM	1441	CA	ASP	202	-13.834	2.923	24.899	1.00	26.03
ATOM	1442	C	ASP	202	-13.386	1.698	24.117	1.00	30.85
ATOM	1443	O	ASP	202	-14.216	0.984	23.546	1.00	30.98
ATOM	1444	CB	ASP	202	-14.654	3.841	23.990	1.00	28.26
ATOM	1445	CG	ASP	202	-15.464	4.848	24.770	1.00	43.04
ATOM	1446	OD1	ASP	202	-16.258	4.401	25.628	1.00	52.14
ATOM	1447	OD2	ASP	202	-15.303	6.060	24.547	1.00	44.22
ATOM	1448	N	THR	203	-12.086	1.451	24.069	1.00	25.69
ATOM	1449	CA	THR	203	-11.587	0.297	23.347	1.00	24.08
ATOM	1450	C	THR	203	-11.707	-0.967	24.179	1.00	28.24
ATOM	1451	O	THR	203	-10.951	-1.189	25.130	1.00	29.39
ATOM	1452	CB	THR	203	-10.145	0.504	22.869	1.00	22.59
ATOM	1453	OG1	THR	203	-10.098	1.685	22.067	1.00	28.88
ATOM	1454	CG2	THR	203	-9.678	-0.665	22.029	1.00	18.61
ATOM	1455	N	GLU	204	-12.760	-1.722	23.891	1.00	23.91
ATOM	1456	CA	GLU	204	-13.028	-2.986	24.560	1.00	24.34
ATOM	1457	C	GLU	204	-12.810	-4.070	23.516	1.00	27.16
ATOM	1458	O	GLU	204	-12.856	-3.820	22.309	1.00	26.99
ATOM	1459	CB	GLU	204	-14.483	-3.091	25.017	1.00	26.97
ATOM	1460	CG	GLU	204	-15.013	-2.054	25.993	1.00	49.92
ATOM	1461	CD	GLU	204	-16.540	-2.055	26.029	1.00	89.01
ATOM	1462	OE1	GLU	204	-17.155	-3.104	25.739	1.00	90.36
ATOM	1463	OE2	GLU	204	-17.127	-0.993	26.318	1.00	92.82
ATOM	1464	N	GLU	205	-12.598	-5.287	23.987	1.00	22.43
ATOM	1465	CA	GLU	205	-12.393	-6.423	23.111	1.00	20.55
ATOM	1466	C	GLU	205	-13.775	-6.929	22.733	1.00	21.14
ATOM	1467	O	GLU	205	-14.668	-6.957	23.574	1.00	17.93
ATOM	1468	CB	GLU	205	-11.610	-7.503	23.850	1.00	22.04
ATOM	1469	CG	GLU	205	-11.100	-8.624	22.991	1.00	32.94
ATOM	1470	CD	GLU	205	-10.167	-9.514	23.763	1.00	51.62
ATOM	1471	OE1	GLU	205	-10.690	-10.332	24.558	1.00	51.06
ATOM	1472	OE2	GLU	205	-8.939	-9.387	23.610	1.00	38.62
ATOM	1473	N	GLU	206	-13.966	-7.296	21.471	1.00	20.25
ATOM	1474	CA	GLU	206	-15.267	-7.780	21.021	1.00	21.26
ATOM	1475	C	GLU	206	-15.158	-8.773	19.859	1.00	24.46
ATOM	1476	O	GLU	206	-14.068	-9.020	19.340	1.00	23.47
ATOM	1477	CB	GLU	206	-16.196	-6.603	20.673	1.00	23.44
ATOM	1478	CG	GLU	206	-16.776	-5.848	21.889	1.00	42.83
ATOM	1479	CD	GLU	206	-16.908	-4.339	21.667	1.00	78.90

ATOM	1480	OE1	GLU	206	-17.346	-3.915	20.577	1.00	98.65
ATOM	1481	OE2	GLU	206	-16.590	-3.576	22.614	1.00	53.79
ATOM	1482	N	ASP	207	-16.302	-9.356	19.496	1.00	21.57
ATOM	1483	CA	ASP	207	-16.437	-10.362	18.430	1.00	21.45
ATOM	1484	C	ASP	207	-16.049	-9.896	17.030	1.00	27.25
ATOM	1485	O	ASP	207	-16.278	-8.748	16.652	1.00	29.30
ATOM	1486	CB	ASP	207	-17.877	-10.885	18.367	1.00	22.21
ATOM	1487	CG	ASP	207	-18.238	-11.775	19.542	1.00	21.70
ATOM	1488	OD1	ASP	207	-17.788	-11.532	20.674	1.00	16.73
ATOM	1489	OD2	ASP	207	-19.024	-12.717	19.330	1.00	33.68
ATOM	1490	N	PHE	208	-15.475	-10.818	16.265	1.00	21.30
ATOM	1491	CA	PHE	208	-15.066	-10.560	14.894	1.00	19.76
ATOM	1492	C	PHE	208	-15.395	-11.810	14.089	1.00	22.95
ATOM	1493	O	PHE	208	-14.783	-12.862	14.262	1.00	22.62
ATOM	1494	CB	PHE	208	-13.577	-10.228	14.786	1.00	21.53
ATOM	1495	CG	PHE	208	-13.176	-9.718	13.424	1.00	23.92
ATOM	1496	CD1	PHE	208	-13.071	-10.586	12.346	1.00	28.21
ATOM	1497	CD2	PHE	208	-12.948	-8.365	13.209	1.00	27.58
ATOM	1498	CE1	PHE	208	-12.747	-10.113	11.072	1.00	31.72
ATOM	1499	CE2	PHE	208	-12.624	-7.885	11.940	1.00	28.80
ATOM	1500	CZ	PHE	208	-12.525	-8.761	10.871	1.00	29.25
ATOM	1501	N	HIS	209	-16.413	-11.687	13.250	1.00	20.52
ATOM	1502	CA	HIS	209	-16.875	-12.769	12.403	1.00	20.85
ATOM	1503	C	HIS	209	-15.919	-13.205	11.306	1.00	23.39
ATOM	1504	O	HIS	209	-15.855	-12.572	10.253	1.00	24.89
ATOM	1505	CB	HIS	209	-18.212	-12.398	11.764	1.00	22.94
ATOM	1506	CG	HIS	209	-19.393	-12.863	12.551	1.00	27.59
ATOM	1507	ND1	HIS	209	-20.195	-13.902	12.127	1.00	30.09
ATOM	1508	CD2	HIS	209	-19.871	-12.478	13.753	1.00	29.90
ATOM	1509	CE1	HIS	209	-21.115	-14.147	13.041	1.00	29.82
ATOM	1510	NE2	HIS	209	-20.940	-13.294	14.041	1.00	30.00
ATOM	1511	N	VAL	210	-15.185	-14.287	11.554	1.00	17.01
ATOM	1512	CA	VAL	210	-14.271	-14.832	10.556	1.00	14.63
ATOM	1513	C	VAL	210	-15.076	-15.769	9.640	1.00	22.79
ATOM	1514	O	VAL	210	-14.609	-16.154	8.563	1.00	24.05
ATOM	1515	CB	VAL	210	-13.113	-15.601	11.203	1.00	15.44
ATOM	1516	CG1	VAL	210	-12.136	-14.616	11.834	1.00	14.45
ATOM	1517	CG2	VAL	210	-13.639	-16.556	12.243	1.00	15.19
ATOM	1518	N	ASP	211	-16.282	-16.129	10.094	1.00	21.95
ATOM	1519	CA	ASP	211	-17.230	-16.992	9.371	1.00	23.32
ATOM	1520	C	ASP	211	-18.628	-16.426	9.607	1.00	30.30
ATOM	1521	O	ASP	211	-18.818	-15.509	10.408	1.00	30.53
ATOM	1522	CB	ASP	211	-17.226	-18.418	9.919	1.00	25.50
ATOM	1523	CG	ASP	211	-16.125	-19.266	9.361	1.00	44.95
ATOM	1524	OD1	ASP	211	-14.933	-18.996	9.608	1.00	48.54
ATOM	1525	OD2	ASP	211	-16.463	-20.274	8.704	1.00	52.49
ATOM	1526	N	GLN	212	-19.622	-17.017	8.960	1.00	29.03
ATOM	1527	CA	GLN	212	-21.007	-16.581	9.148	1.00	29.12
ATOM	1528	C	GLN	212	-21.484	-17.190	10.451	1.00	34.30
ATOM	1529	O	GLN	212	-22.502	-16.770	10.992	1.00	36.41
ATOM	1530	CB	GLN	212	-21.918	-17.103	8.026	1.00	30.36
ATOM	1531	CG	GLN	212	-21.633	-16.563	6.630	1.00	49.34
ATOM	1532	CD	GLN	212	-22.656	-15.539	6.172	1.00	64.74
ATOM	1533	OE1	GLN	212	-23.716	-15.377	6.779	1.00	59.48

ATOM	1534	NE2	GLN	212	-22.340	-14.839	5.091	1.00	56.91
ATOM	1535	N	VAL	213	-20.726	-18.166	10.950	1.00	28.15
ATOM	1536	CA	VAL	213	-21.077	-18.876	12.178	1.00	25.98
ATOM	1537	C	VAL	213	-19.956	-18.912	13.220	1.00	26.83
ATOM	1538	O	VAL	213	-20.164	-19.375	14.339	1.00	24.65
ATOM	1539	CB	VAL	213	-21.491	-20.338	11.870	1.00	28.98
ATOM	1540	CG1	VAL	213	-22.700	-20.351	10.956	1.00	28.50
ATOM	1541	CG2	VAL	213	-20.327	-21.109	11.243	1.00	28.77
ATOM	1542	N	THR	214	-18.784	-18.409	12.851	1.00	23.26
ATOM	1543	CA	THR	214	-17.641	-18.411	13.747	1.00	23.15
ATOM	1544	C	THR	214	-17.196	-16.989	14.050	1.00	27.67
ATOM	1545	O	THR	214	-17.353	-16.090	13.221	1.00	27.31
ATOM	1546	CB	THR	214	-16.461	-19.186	13.136	1.00	31.51
ATOM	1547	OG1	THR	214	-16.968	-20.276	12.347	1.00	28.47
ATOM	1548	CG2	THR	214	-15.551	-19.727	14.227	1.00	32.93
ATOM	1549	N	THR	215	-16.665	-16.793	15.250	1.00	25.25
ATOM	1550	CA	THR	215	-16.198	-15.496	15.694	1.00	25.06
ATOM	1551	C	THR	215	-14.836	-15.607	16.353	1.00	26.60
ATOM	1552	O	THR	215	-14.365	-16.697	16.655	1.00	26.58
ATOM	1553	CB	THR	215	-17.187	-14.856	16.708	1.00	39.80
ATOM	1554	OG1	THR	215	-17.476	-15.787	17.760	1.00	40.04
ATOM	1555	CG2	THR	215	-18.480	-14.468	16.029	1.00	43.19
ATOM	1556	N	VAL	216	-14.205	-14.458	16.537	1.00	21.12
ATOM	1557	CA	VAL	216	-12.907	-14.343	17.166	1.00	19.03
ATOM	1558	C	VAL	216	-12.933	-13.000	17.890	1.00	26.31
ATOM	1559	O	VAL	216	-13.723	-12.118	17.550	1.00	26.92
ATOM	1560	CB	VAL	216	-11.782	-14.408	16.122	1.00	20.18
ATOM	1561	CG1	VAL	216	-10.557	-13.656	16.590	1.00	19.92
ATOM	1562	CG2	VAL	216	-11.434	-15.852	15.873	1.00	19.39
ATOM	1563	N	LYS	217	-12.159	-12.889	18.962	1.00	23.35
ATOM	1564	CA	LYS	217	-12.119	-11.660	19.734	1.00	23.09
ATOM	1565	C	LYS	217	-10.944	-10.809	19.295	1.00	24.17
ATOM	1566	O	LYS	217	-9.854	-11.320	19.004	1.00	21.99
ATOM	1567	CB	LYS	217	-12.028	-11.978	21.226	1.00	27.15
ATOM	1568	CG	LYS	217	-13.130	-12.891	21.712	1.00	34.17
ATOM	1569	CD	LYS	217	-14.487	-12.239	21.553	1.00	37.75
ATOM	1570	CE	LYS	217	-15.602	-13.250	21.705	1.00	51.12
ATOM	1571	NZ	LYS	217	-15.661	-14.121	20.501	1.00	59.22
ATOM	1572	N	VAL	218	-11.194	-9.509	19.216	1.00	20.37
ATOM	1573	CA	VAL	218	-10.183	-8.538	18.823	1.00	19.85
ATOM	1574	C	VAL	218	-10.486	-7.236	19.547	1.00	19.60
ATOM	1575	O	VAL	218	-11.622	-7.030	19.985	1.00	19.43
ATOM	1576	CB	VAL	218	-10.225	-8.280	17.295	1.00	25.31
ATOM	1577	CG1	VAL	218	-9.764	-9.521	16.540	1.00	26.00
ATOM	1578	CG2	VAL	218	-11.625	-7.885	16.853	1.00	24.90
ATOM	1579	N	PRO	219	-9.457	-6.414	19.824	1.00	14.76
ATOM	1580	CA	PRO	219	-9.675	-5.138	20.509	1.00	15.37
ATOM	1581	C	PRO	219	-10.433	-4.208	19.567	1.00	19.72
ATOM	1582	O	PRO	219	-9.870	-3.689	18.594	1.00	22.88
ATOM	1583	CB	PRO	219	-8.258	-4.635	20.760	1.00	16.67
ATOM	1584	CG	PRO	219	-7.487	-5.238	19.644	1.00	20.99
ATOM	1585	CD	PRO	219	-8.020	-6.646	19.644	1.00	15.91
ATOM	1586	N	MET	220	-11.700	-3.990	19.892	1.00	10.54
ATOM	1587	CA	MET	220	-12.589	-3.173	19.097	1.00	7.76

ATOM	1588	C	MET	220	-12.674	-1.738	19.586	1.00	9.93
ATOM	1589	O	MET	220	-13.041	-1.473	20.729	1.00	12.28
ATOM	1590	CB	MET	220	-13.982	-3.801	19.098	1.00	9.32
ATOM	1591	CG	MET	220	-14.911	-3.270	18.038	1.00	12.33
ATOM	1592	SD	MET	220	-14.409	-3.705	16.384	1.00	15.68
ATOM	1593	CE	MET	220	-14.740	-5.479	16.336	1.00	12.17
ATOM	1594	N	MET	221	-12.302	-0.813	18.717	1.00	4.18
ATOM	1595	CA	MET	221	-12.378	0.600	19.036	1.00	3.81
ATOM	1596	C	MET	221	-13.821	1.013	18.717	1.00	8.98
ATOM	1597	O	MET	221	-14.500	0.347	17.929	1.00	7.18
ATOM	1598	CB	MET	221	-11.407	1.403	18.152	1.00	5.88
ATOM	1599	CG	MET	221	-9.995	0.842	18.045	1.00	8.69
ATOM	1600	SD	MET	221	-8.838	1.916	17.171	1.00	11.36
ATOM	1601	CE	MET	221	-9.315	1.597	15.511	1.00	8.44
ATOM	1602	N	LYS	222	-14.306	2.075	19.355	1.00	9.02
ATOM	1603	CA	LYS	222	-15.655	2.573	19.089	1.00	10.15
ATOM	1604	C	LYS	222	-15.826	4.059	19.387	1.00	12.60
ATOM	1605	O	LYS	222	-15.204	4.594	20.306	1.00	12.75
ATOM	1606	CB	LYS	222	-16.714	1.743	19.823	1.00	15.09
ATOM	1607	CG	LYS	222	-16.512	1.603	21.314	1.00	37.80
ATOM	1608	CD	LYS	222	-17.741	0.947	21.923	1.00	50.19
ATOM	1609	CE	LYS	222	-17.542	0.621	23.389	1.00	62.83
ATOM	1610	NZ	LYS	222	-16.475	-0.403	23.522	1.00	62.90
ATOM	1611	N	ARG	223	-16.682	4.698	18.567	1.00	7.78
ATOM	1612	CA	ARG	223	-16.903	6.122	18.728	1.00	7.43
ATOM	1613	C	ARG	223	-18.216	6.507	18.106	1.00	14.04
ATOM	1614	O	ARG	223	-18.471	6.190	16.955	1.00	14.71
ATOM	1615	CB	ARG	223	-15.760	6.919	18.065	1.00	1.85
ATOM	1616	CG	ARG	223	-16.002	8.432	18.236	1.00	8.27
ATOM	1617	CD	ARG	223	-14.808	9.222	17.674	1.00	12.86
ATOM	1618	NE	ARG	223	-14.917	9.339	16.230	1.00	21.24
ATOM	1619	CZ	ARG	223	-15.401	10.410	15.670	1.00	39.54
ATOM	1620	NH1	ARG	223	-15.826	11.415	16.381	1.00	21.45
ATOM	1621	NH2	ARG	223	-15.459	10.480	14.373	1.00	36.93
ATOM	1622	N	LEU	224	-19.051	7.207	18.895	1.00	11.24
ATOM	1623	CA	LEU	224	-20.281	7.729	18.333	1.00	11.34
ATOM	1624	C	LEU	224	-19.992	9.123	17.859	1.00	17.43
ATOM	1625	O	LEU	224	-19.508	9.931	18.636	1.00	19.15
ATOM	1626	CB	LEU	224	-21.364	7.768	19.430	1.00	11.10
ATOM	1627	CG	LEU	224	-22.618	8.519	18.940	1.00	14.59
ATOM	1628	CD1	LEU	224	-23.329	7.707	17.843	1.00	14.40
ATOM	1629	CD2	LEU	224	-23.576	8.750	20.122	1.00	16.42
ATOM	1630	N	GLY	225	-20.287	9.408	16.577	1.00	14.04
ATOM	1631	CA	GLY	225	-20.017	10.748	16.092	1.00	13.48
ATOM	1632	C	GLY	225	-20.422	10.920	14.656	1.00	19.70
ATOM	1633	O	GLY	225	-21.026	10.042	14.062	1.00	22.63
ATOM	1634	N	MET	226	-20.071	12.100	14.109	1.00	11.91
ATOM	1635	CA	MET	226	-20.423	12.382	12.730	1.00	8.35
ATOM	1636	C	MET	226	-19.364	11.799	11.838	1.00	11.83
ATOM	1637	O	MET	226	-18.303	12.383	11.677	1.00	10.56
ATOM	1638	CB	MET	226	-20.518	13.910	12.539	1.00	8.55
ATOM	1639	CG	MET	226	-21.405	14.548	13.627	1.00	9.32
ATOM	1640	SD	MET	226	-23.076	13.833	13.531	1.00	10.74
ATOM	1641	CE	MET	226	-23.518	14.429	11.871	1.00	6.35

ATOM	1642	N	PHE	227	-19.665	10.623	11.255	1.00	8.57
ATOM	1643	CA	PHE	227	-18.691	10.000	10.378	1.00	8.12
ATOM	1644	C	PHE	227	-19.003	10.264	8.931	1.00	13.66
ATOM	1645	O	PHE	227	-20.135	10.556	8.580	1.00	12.48
ATOM	1646	CB	PHE	227	-18.639	8.479	10.625	1.00	8.75
ATOM	1647	CG	PHE	227	-18.070	8.192	12.012	1.00	8.71
ATOM	1648	CD1	PHE	227	-16.694	8.013	12.177	1.00	9.74
ATOM	1649	CD2	PHE	227	-18.923	8.102	13.116	1.00	9.32
ATOM	1650	CE1	PHE	227	-16.174	7.720	13.440	1.00	11.09
ATOM	1651	CE2	PHE	227	-18.402	7.823	14.381	1.00	8.85
ATOM	1652	CZ	PHE	227	-17.028	7.622	14.542	1.00	8.29
ATOM	1653	N	ASN	228	-17.960	10.148	8.086	1.00	12.09
ATOM	1654	CA	ASN	228	-18.159	10.287	6.642	1.00	11.99
ATOM	1655	C	ASN	228	-18.533	8.882	6.173	1.00	19.62
ATOM	1656	O	ASN	228	-17.936	8.345	5.243	1.00	21.62
ATOM	1657	CB	ASN	228	-16.860	10.754	5.968	1.00	7.09
ATOM	1658	CG	ASN	228	-17.041	11.137	4.498	1.00	20.29
ATOM	1659	OD1	ASN	228	-16.219	11.868	3.946	1.00	21.94
ATOM	1660	ND2	ASN	228	-18.085	10.619	3.850	1.00	11.18
ATOM	1661	N	ILE	229	-19.525	8.303	6.841	1.00	16.46
ATOM	1662	CA	ILE	229	-20.001	6.958	6.565	1.00	16.35
ATOM	1663	C	ILE	229	-21.244	6.990	5.687	1.00	18.71
ATOM	1664	O	ILE	229	-22.059	7.907	5.771	1.00	16.82
ATOM	1665	CB	ILE	229	-20.336	6.227	7.890	1.00	20.15
ATOM	1666	CG1	ILE	229	-20.764	4.780	7.631	1.00	21.22
ATOM	1667	CG2	ILE	229	-21.461	6.970	8.634	1.00	21.83
ATOM	1668	CD1	ILE	229	-19.660	3.886	7.182	1.00	35.66
ATOM	1669	N	GLN	230	-21.374	5.974	4.845	1.00	16.88
ATOM	1670	CA	GLN	230	-22.505	5.830	3.939	1.00	16.55
ATOM	1671	C	GLN	230	-22.645	4.362	3.585	1.00	20.45
ATOM	1672	O	GLN	230	-21.793	3.558	3.938	1.00	19.02
ATOM	1673	CB	GLN	230	-22.339	6.675	2.654	1.00	17.31
ATOM	1674	CG	GLN	230	-20.974	6.615	1.965	1.00	26.85
ATOM	1675	CD	GLN	230	-19.968	7.619	2.529	1.00	46.34
ATOM	1676	OE1	GLN	230	-18.755	7.377	2.537	1.00	38.32
ATOM	1677	NE2	GLN	230	-20.473	8.748	3.011	1.00	44.00
ATOM	1678	N	HIS	231	-23.752	4.010	2.945	1.00	19.04
ATOM	1679	CA	HIS	231	-23.979	2.641	2.538	1.00	19.99
ATOM	1680	C	HIS	231	-24.244	2.618	1.047	1.00	25.53
ATOM	1681	O	HIS	231	-25.347	2.942	0.594	1.00	25.20
ATOM	1682	CB	HIS	231	-25.158	2.015	3.277	1.00	21.24
ATOM	1683	CG	HIS	231	-25.361	0.571	2.938	1.00	25.66
ATOM	1684	ND1	HIS	231	-25.989	0.157	1.784	1.00	28.29
ATOM	1685	CD2	HIS	231	-24.980	-0.551	3.585	1.00	29.45
ATOM	1686	CE1	HIS	231	-25.984	-1.165	1.726	1.00	29.07
ATOM	1687	NE2	HIS	231	-25.376	-1.617	2.814	1.00	29.87
ATOM	1688	N	CYS	232	-23.230	2.227	0.292	1.00	23.51
ATOM	1689	CA	CYS	232	-23.335	2.162	-1.151	1.00	24.24
ATOM	1690	C	CYS	232	-24.054	0.898	-1.592	1.00	28.94
ATOM	1691	O	CYS	232	-23.603	-0.216	-1.319	1.00	27.88
ATOM	1692	CB	CYS	232	-21.946	2.190	-1.780	1.00	25.39
ATOM	1693	SG	CYS	232	-21.982	2.445	-3.578	1.00	30.39
ATOM	1694	N	LYS	233	-25.186	1.064	-2.260	1.00	27.44
ATOM	1695	CA	LYS	233	-25.913	-0.094	-2.747	1.00	28.83

ATOM	1696	C	LYS	233	-25.143	-0.759	-3.884	1.00	35.28
ATOM	1697	O	LYS	233	-25.045	-1.985	-3.931	1.00	35.85
ATOM	1698	CB	LYS	233	-27.324	0.279	-3.204	1.00	31.74
ATOM	1699	CG	LYS	233	-28.321	0.486	-2.068	1.00	52.69
ATOM	1700	CD	LYS	233	-28.466	-0.750	-1.195	1.00	58.67
ATOM	1701	CE	LYS	233	-29.501	-0.548	-0.108	1.00	67.74
ATOM	1702	NZ	LYS	233	-29.592	-1.712	0.805	1.00	73.46
ATOM	1703	N	LYS	234	-24.536	0.049	-4.753	1.00	31.86
ATOM	1704	CA	LYS	234	-23.780	-0.488	-5.878	1.00	31.67
ATOM	1705	C	LYS	234	-22.698	-1.456	-5.434	1.00	34.72
ATOM	1706	O	LYS	234	-22.536	-2.517	-6.023	1.00	36.21
ATOM	1707	CB	LYS	234	-23.158	0.627	-6.713	1.00	35.04
ATOM	1708	CG	LYS	234	-22.409	0.109	-7.938	1.00	49.04
ATOM	1709	CD	LYS	234	-22.403	1.126	-9.065	1.00	59.59
ATOM	1710	CE	LYS	234	-22.003	0.484	-10.385	1.00	61.46
ATOM	1711	NZ	LYS	234	-22.208	1.403	-11.533	1.00	64.53
ATOM	1712	N	LEU	235	-21.951	-1.088	-4.404	1.00	27.51
ATOM	1713	CA	LEU	235	-20.893	-1.949	-3.904	1.00	25.46
ATOM	1714	C	LEU	235	-21.446	-2.913	-2.859	1.00	27.92
ATOM	1715	O	LEU	235	-20.745	-3.816	-2.412	1.00	27.78
ATOM	1716	CB	LEU	235	-19.767	-1.108	-3.297	1.00	25.05
ATOM	1717	CG	LEU	235	-19.005	-0.163	-4.226	1.00	29.21
ATOM	1718	CD1	LEU	235	-18.113	0.743	-3.424	1.00	29.02
ATOM	1719	CD2	LEU	235	-18.198	-0.946	-5.225	1.00	34.69
ATOM	1720	N	SER	236	-22.717	-2.751	-2.518	1.00	24.49
ATOM	1721	CA	SER	236	-23.363	-3.593	-1.518	1.00	25.00
ATOM	1722	C	SER	236	-22.546	-3.589	-0.229	1.00	26.77
ATOM	1723	O	SER	236	-22.227	-4.649	0.326	1.00	27.44
ATOM	1724	CB	SER	236	-23.533	-5.025	-2.033	1.00	31.15
ATOM	1725	OG	SER	236	-24.358	-5.069	-3.188	1.00	47.28
ATOM	1726	N	SER	237	-22.230	-2.392	0.260	1.00	19.80
ATOM	1727	CA	SER	237	-21.440	-2.266	1.474	1.00	17.87
ATOM	1728	C	SER	237	-21.371	-0.879	2.096	1.00	17.31
ATOM	1729	O	SER	237	-21.623	0.124	1.440	1.00	15.81
ATOM	1730	CB	SER	237	-20.021	-2.774	1.212	1.00	21.38
ATOM	1731	OG	SER	237	-19.642	-2.578	-0.137	1.00	30.13
ATOM	1732	N	TRP	238	-21.085	-0.842	3.391	1.00	12.22
ATOM	1733	CA	TRP	238	-20.928	0.407	4.112	1.00	11.25
ATOM	1734	C	TRP	238	-19.531	0.929	3.774	1.00	13.06
ATOM	1735	O	TRP	238	-18.538	0.193	3.867	1.00	11.46
ATOM	1736	CB	TRP	238	-21.015	0.167	5.612	1.00	11.29
ATOM	1737	CG	TRP	238	-22.403	0.081	6.189	1.00	13.72
ATOM	1738	CD1	TRP	238	-23.086	-1.049	6.529	1.00	16.79
ATOM	1739	CD2	TRP	238	-23.214	1.183	6.607	1.00	13.82
ATOM	1740	NE1	TRP	238	-24.272	-0.716	7.135	1.00	15.81
ATOM	1741	CE2	TRP	238	-24.382	0.638	7.180	1.00	16.81
ATOM	1742	CE3	TRP	238	-23.076	2.568	6.527	1.00	15.44
ATOM	1743	CZ2	TRP	238	-25.386	1.444	7.709	1.00	15.82
ATOM	1744	CZ3	TRP	238	-24.076	3.364	7.053	1.00	16.61
ATOM	1745	CH2	TRP	238	-25.227	2.799	7.620	1.00	16.65
ATOM	1746	N	VAL	239	-19.475	2.183	3.341	1.00	9.68
ATOM	1747	CA	VAL	239	-18.231	2.852	2.968	1.00	8.63
ATOM	1748	C	VAL	239	-17.942	4.013	3.944	1.00	10.72
ATOM	1749	O	VAL	239	-18.667	5.011	3.981	1.00	6.54

ATOM	1750	CB	VAL	239	-18.320	3.369	1.507	1.00	12.66
ATOM	1751	CG1	VAL	239	-17.017	4.042	1.084	1.00	12.90
ATOM	1752	CG2	VAL	239	-18.671	2.225	0.579	1.00	12.01
ATOM	1753	N	LEU	240	-16.871	3.849	4.720	1.00	10.01
ATOM	1754	CA	LEU	240	-16.427	4.799	5.737	1.00	10.33
ATOM	1755	C	LEU	240	-15.128	5.523	5.387	1.00	15.02
ATOM	1756	O	LEU	240	-14.099	4.884	5.166	1.00	14.95
ATOM	1757	CB	LEU	240	-16.229	4.051	7.057	1.00	10.48
ATOM	1758	CG	LEU	240	-15.548	4.799	8.203	1.00	16.26
ATOM	1759	CD1	LEU	240	-16.472	5.855	8.781	1.00	17.63
ATOM	1760	CD2	LEU	240	-15.124	3.817	9.263	1.00	15.41
ATOM	1761	N	LEU	241	-15.164	6.850	5.366	1.00	12.02
ATOM	1762	CA	LEU	241	-13.962	7.620	5.070	1.00	12.27
ATOM	1763	C	LEU	241	-13.329	8.283	6.298	1.00	18.80
ATOM	1764	O	LEU	241	-13.777	9.334	6.774	1.00	18.43
ATOM	1765	CB	LEU	241	-14.214	8.648	3.964	1.00	11.42
ATOM	1766	CG	LEU	241	-14.176	8.089	2.541	1.00	15.05
ATOM	1767	CD1	LEU	241	-15.379	7.211	2.276	1.00	15.36
ATOM	1768	CD2	LEU	241	-14.119	9.229	1.547	1.00	16.74
ATOM	1769	N	MET	242	-12.284	7.641	6.806	1.00	17.21
ATOM	1770	CA	MET	242	-11.544	8.120	7.967	1.00	18.01
ATOM	1771	C	MET	242	-10.409	9.053	7.550	1.00	23.47
ATOM	1772	O	MET	242	-9.468	8.668	6.864	1.00	24.19
ATOM	1773	CB	MET	242	-10.966	6.950	8.766	1.00	20.26
ATOM	1774	CG	MET	242	-11.988	6.085	9.455	1.00	22.94
ATOM	1775	SD	MET	242	-12.629	6.786	10.951	1.00	25.83
ATOM	1776	CE	MET	242	-11.268	6.581	12.006	1.00	22.11
ATOM	1777	N	LYS	243	-10.562	10.302	8.032	1.00	18.99
ATOM	1778	CA	LYS	243	-9.548	11.312	7.802	1.00	17.66
ATOM	1779	C	LYS	243	-8.317	11.048	8.622	1.00	17.67
ATOM	1780	O	LYS	243	-8.398	10.740	9.802	1.00	18.08
ATOM	1781	CB	LYS	243	-10.105	12.714	8.132	1.00	21.90
ATOM	1782	CG	LYS	243	-10.690	12.755	9.559	1.00	25.80
ATOM	1783	CD	LYS	243	-12.103	12.137	9.582	1.00	18.62
ATOM	1784	CE	LYS	243	-12.461	11.654	11.002	1.00	26.35
ATOM	1785	NZ	LYS	243	-13.822	11.096	11.020	1.00	23.36
ATOM	1786	N	TYR	244	-7.159	11.177	7.954	1.00	13.01
ATOM	1787	CA	TYR	244	-5.890	10.998	8.667	1.00	12.02
ATOM	1788	C	TYR	244	-5.195	12.310	8.951	1.00	19.96
ATOM	1789	O	TYR	244	-5.138	13.207	8.100	1.00	20.97
ATOM	1790	CB	TYR	244	-4.898	10.149	7.870	1.00	11.09
ATOM	1791	CG	TYR	244	-4.867	8.706	8.243	1.00	12.20
ATOM	1792	CD1	TYR	244	-4.636	8.316	9.553	1.00	12.28
ATOM	1793	CD2	TYR	244	-5.089	7.722	7.285	1.00	14.62
ATOM	1794	CE1	TYR	244	-4.637	6.974	9.901	1.00	13.09
ATOM	1795	CE2	TYR	244	-5.089	6.376	7.624	1.00	12.96
ATOM	1796	CZ	TYR	244	-4.864	6.016	8.927	1.00	23.64
ATOM	1797	OH	TYR	244	-4.858	4.692	9.255	1.00	34.09
ATOM	1798	N	LEU	245	-4.618	12.389	10.141	1.00	18.61
ATOM	1799	CA	LEU	245	-3.873	13.559	10.553	1.00	19.17
ATOM	1800	C	LEU	245	-2.578	13.463	9.768	1.00	28.06
ATOM	1801	O	LEU	245	-1.675	12.710	10.122	1.00	29.74
ATOM	1802	CB	LEU	245	-3.586	13.518	12.056	1.00	18.84
ATOM	1803	CG	LEU	245	-2.913	14.754	12.632	1.00	22.04

ATOM	1804	CD1	LEU	245	-3.868	15.926	12.519	1.00	21.70
ATOM	1805	CD2	LEU	245	-2.503	14.504	14.070	1.00	21.91
ATOM	1806	N	GLY	246	-2.544	14.157	8.644	1.00	27.56
ATOM	1807	CA	GLY	246	-1.381	14.155	7.782	1.00	28.42
ATOM	1808	C	GLY	246	-1.875	14.635	6.435	1.00	34.25
ATOM	1809	O	GLY	246	-2.143	15.817	6.252	1.00	38.08
ATOM	1810	N	ASN	247	-2.098	13.712	5.517	1.00	26.63
ATOM	1811	CA	ASN	247	-2.575	14.073	4.198	1.00	24.75
ATOM	1812	C	ASN	247	-3.077	12.827	3.491	1.00	24.56
ATOM	1813	O	ASN	247	-3.054	12.741	2.262	1.00	23.68
ATOM	1814	CB	ASN	247	-1.458	14.745	3.388	1.00	26.63
ATOM	1815	CG	ASN	247	-0.157	13.956	3.414	1.00	38.57
ATOM	1816	OD1	ASN	247	0.368	13.645	4.487	1.00	45.16
ATOM	1817	ND2	ASN	247	0.373	13.637	2.237	1.00	10.21
ATOM	1818	N	ALA	248	-3.538	11.863	4.276	1.00	19.01
ATOM	1819	CA	ALA	248	-4.063	10.619	3.735	1.00	18.29
ATOM	1820	C	ALA	248	-5.469	10.366	4.300	1.00	17.56
ATOM	1821	O	ALA	248	-5.809	10.858	5.377	1.00	14.85
ATOM	1822	CB	ALA	248	-3.125	9.458	4.064	1.00	19.31
ATOM	1823	N	THR	249	-6.286	9.648	3.535	1.00	11.98
ATOM	1824	CA	THR	249	-7.651	9.314	3.912	1.00	9.23
ATOM	1825	C	THR	249	-7.837	7.808	3.810	1.00	11.01
ATOM	1826	O	THR	249	-7.495	7.187	2.808	1.00	9.71
ATOM	1827	CB	THR	249	-8.689	10.012	2.996	1.00	5.40
ATOM	1828	OG1	THR	249	-8.623	11.435	3.175	1.00	6.92
ATOM	1829	CG2	THR	249	-10.098	9.525	3.302	1.00	1.00
ATOM	1830	N	ALA	250	-8.331	7.233	4.891	1.00	7.89
ATOM	1831	CA	ALA	250	-8.601	5.819	5.001	1.00	7.37
ATOM	1832	C	ALA	250	-10.008	5.556	4.497	1.00	11.92
ATOM	1833	O	ALA	250	-10.950	6.222	4.927	1.00	14.56
ATOM	1834	CB	ALA	250	-8.504	5.396	6.468	1.00	7.88
ATOM	1835	N	ILE	251	-10.146	4.646	3.542	1.00	5.32
ATOM	1836	CA	ILE	251	-11.457	4.273	3.030	1.00	3.97
ATOM	1837	C	ILE	251	-11.611	2.810	3.441	1.00	6.37
ATOM	1838	O	ILE	251	-10.709	1.998	3.225	1.00	6.05
ATOM	1839	CB	ILE	251	-11.564	4.365	1.483	1.00	7.21
ATOM	1840	CG1	ILE	251	-11.090	5.725	0.970	1.00	6.26
ATOM	1841	CG2	ILE	251	-13.007	4.160	1.052	1.00	10.19
ATOM	1842	CD1	ILE	251	-11.354	5.922	-0.507	1.00	1.00
ATOM	1843	N	PHE	252	-12.714	2.501	4.112	1.00	1.97
ATOM	1844	CA	PHE	252	-13.006	1.147	4.572	1.00	1.00
ATOM	1845	C	PHE	252	-14.298	0.701	3.928	1.00	7.08
ATOM	1846	O	PHE	252	-15.267	1.458	3.893	1.00	8.36
ATOM	1847	CB	PHE	252	-13.196	1.112	6.094	1.00	1.68
ATOM	1848	CG	PHE	252	-11.989	1.534	6.877	1.00	1.01
ATOM	1849	CD1	PHE	252	-10.907	0.676	7.019	1.00	2.49
ATOM	1850	CD2	PHE	252	-11.936	2.785	7.466	1.00	1.00
ATOM	1851	CE1	PHE	252	-9.792	1.052	7.745	1.00	2.81
ATOM	1852	CE2	PHE	252	-10.827	3.169	8.192	1.00	4.34
ATOM	1853	CZ	PHE	252	-9.745	2.302	8.328	1.00	2.20
ATOM	1854	N	PHE	253	-14.333	-0.556	3.507	1.00	3.93
ATOM	1855	CA	PHE	253	-15.503	-1.110	2.858	1.00	4.58
ATOM	1856	C	PHE	253	-15.964	-2.354	3.599	1.00	13.67
ATOM	1857	O	PHE	253	-15.284	-3.388	3.571	1.00	11.49

ATOM	1858	CB	PHE	253	-15.174	-1.500	1.415	1.00	5.96
ATOM	1859	CG	PHE	253	-14.641	-0.377	0.577	1.00	7.08
ATOM	1860	CD1	PHE	253	-15.509	0.475	-0.095	1.00	8.18
ATOM	1861	CD2	PHE	253	-13.274	-0.162	0.465	1.00	10.35
ATOM	1862	CE1	PHE	253	-15.021	1.526	-0.863	1.00	10.14
ATOM	1863	CE2	PHE	253	-12.781	0.886	-0.301	1.00	10.64
ATOM	1864	CZ	PHE	253	-13.657	1.733	-0.965	1.00	8.11
ATOM	1865	N	LEU	254	-17.142	-2.265	4.212	1.00	15.28
ATOM	1866	CA	LEU	254	-17.736	-3.383	4.954	1.00	15.29
ATOM	1867	C	LEU	254	-18.796	-4.004	4.053	1.00	19.45
ATOM	1868	O	LEU	254	-19.908	-3.482	3.949	1.00	20.52
ATOM	1869	CB	LEU	254	-18.372	-2.888	6.259	1.00	14.77
ATOM	1870	CG	LEU	254	-18.943	-3.951	7.192	1.00	18.06
ATOM	1871	CD1	LEU	254	-17.835	-4.910	7.607	1.00	18.39
ATOM	1872	CD2	LEU	254	-19.564	-3.267	8.400	1.00	17.27
ATOM	1873	N	PRO	255	-18.459	-5.110	3.371	1.00	14.39
ATOM	1874	CA	PRO	255	-19.415	-5.765	2.483	1.00	14.37
ATOM	1875	C	PRO	255	-20.653	-6.289	3.215	1.00	22.98
ATOM	1876	O	PRO	255	-20.571	-6.721	4.370	1.00	23.70
ATOM	1877	CB	PRO	255	-18.596	-6.902	1.905	1.00	15.27
ATOM	1878	CG	PRO	255	-17.692	-7.268	3.041	1.00	18.40
ATOM	1879	CD	PRO	255	-17.225	-5.914	3.481	1.00	13.45
ATOM	1880	N	ASP	256	-21.794	-6.268	2.532	1.00	19.61
ATOM	1881	CA	ASP	256	-23.057	-6.740	3.108	1.00	18.85
ATOM	1882	C	ASP	256	-22.960	-8.236	3.426	1.00	24.45
ATOM	1883	O	ASP	256	-21.892	-8.839	3.325	1.00	24.28
ATOM	1884	CB	ASP	256	-24.249	-6.440	2.169	1.00	19.61
ATOM	1885	CG	ASP	256	-24.732	-4.970	2.262	1.00	23.84
ATOM	1886	OD1	ASP	256	-24.129	-4.149	2.985	1.00	20.06
ATOM	1887	OD2	ASP	256	-25.730	-4.635	1.570	1.00	31.51
ATOM	1888	N	GLU	257	-24.057	-8.818	3.893	1.00	23.21
ATOM	1889	CA	GLU	257	-24.068	-10.240	4.214	1.00	23.79
ATOM	1890	C	GLU	257	-23.779	-10.976	2.909	1.00	26.24
ATOM	1891	O	GLU	257	-24.541	-10.862	1.953	1.00	24.82
ATOM	1892	CB	GLU	257	-25.443	-10.629	4.756	1.00	25.85
ATOM	1893	CG	GLU	257	-25.538	-11.987	5.444	1.00	41.87
ATOM	1894	CD	GLU	257	-26.943	-12.273	5.968	1.00	72.26
ATOM	1895	OE1	GLU	257	-27.634	-11.331	6.418	1.00	76.34
ATOM	1896	OE2	GLU	257	-27.352	-13.454	5.927	1.00	67.23
ATOM	1897	N	GLY	258	-22.613	-11.613	2.839	1.00	23.16
ATOM	1898	CA	GLY	258	-22.228	-12.362	1.648	1.00	22.95
ATOM	1899	C	GLY	258	-21.875	-11.549	0.407	1.00	28.21
ATOM	1900	O	GLY	258	-21.772	-12.107	-0.685	1.00	30.38
ATOM	1901	N	LYS	259	-21.645	-10.247	0.561	1.00	21.62
ATOM	1902	CA	LYS	259	-21.319	-9.397	-0.581	1.00	19.47
ATOM	1903	C	LYS	259	-19.854	-8.959	-0.663	1.00	21.82
ATOM	1904	O	LYS	259	-19.564	-7.857	-1.134	1.00	21.44
ATOM	1905	CB	LYS	259	-22.233	-8.171	-0.595	1.00	21.50
ATOM	1906	CG	LYS	259	-23.669	-8.469	-0.980	1.00	25.83
ATOM	1907	CD	LYS	259	-23.822	-8.619	-2.472	1.00	29.92
ATOM	1908	CE	LYS	259	-25.263	-8.844	-2.885	1.00	37.09
ATOM	1909	NZ	LYS	259	-25.394	-8.979	-4.358	1.00	46.52
ATOM	1910	N	LEU	260	-18.924	-9.825	-0.262	1.00	16.31
ATOM	1911	CA	LEU	260	-17.500	-9.474	-0.322	1.00	14.94

ATOM	1912	C	LEU	260	-16.929	-9.593	-1.732	1.00	26.00
ATOM	1913	O	LEU	260	-16.263	-8.677	-2.213	1.00	27.32
ATOM	1914	CB	LEU	260	-16.667	-10.294	0.672	1.00	12.73
ATOM	1915	CG	LEU	260	-15.138	-10.131	0.721	1.00	13.73
ATOM	1916	CD1	LEU	260	-14.696	-8.701	0.938	1.00	11.63
ATOM	1917	CD2	LEU	260	-14.611	-11.018	1.820	1.00	16.86
ATOM	1918	N	GLN	261	-17.239	-10.688	-2.414	1.00	25.25
ATOM	1919	CA	GLN	261	-16.743	-10.894	-3.775	1.00	27.07
ATOM	1920	C	GLN	261	-17.251	-9.774	-4.693	1.00	30.23
ATOM	1921	O	GLN	261	-16.502	-9.238	-5.508	1.00	32.36
ATOM	1922	CB	GLN	261	-17.181	-12.266	-4.303	1.00	29.06
ATOM	1923	CG	GLN	261	-16.633	-12.612	-5.683	1.00	46.56
ATOM	1924	CD	GLN	261	-15.127	-12.692	-5.719	1.00	84.32
ATOM	1925	OE1	GLN	261	-14.447	-12.444	-4.724	1.00	84.95
ATOM	1926	NE2	GLN	261	-14.592	-13.051	-6.873	1.00	87.30
ATOM	1927	N	HIS	262	-18.509	-9.392	-4.495	1.00	21.14
ATOM	1928	CA	HIS	262	-19.147	-8.333	-5.259	1.00	18.96
ATOM	1929	C	HIS	262	-18.394	-7.009	-5.079	1.00	20.50
ATOM	1930	O	HIS	262	-18.037	-6.354	-6.052	1.00	19.00
ATOM	1931	CB	HIS	262	-20.600	-8.177	-4.791	1.00	19.08
ATOM	1932	CG	HIS	262	-21.325	-7.025	-5.418	1.00	21.74
ATOM	1933	ND1	HIS	262	-22.215	-7.191	-6.455	1.00	23.34
ATOM	1934	CD2	HIS	262	-21.298	-5.701	-5.154	1.00	23.53
ATOM	1935	CE1	HIS	262	-22.707	-6.018	-6.810	1.00	22.73
ATOM	1936	NE2	HIS	262	-22.163	-5.096	-6.034	1.00	23.15
ATOM	1937	N	LEU	263	-18.170	-6.622	-3.829	1.00	15.36
ATOM	1938	CA	LEU	263	-17.460	-5.391	-3.533	1.00	14.39
ATOM	1939	C	LEU	263	-16.122	-5.351	-4.261	1.00	18.62
ATOM	1940	O	LEU	263	-15.841	-4.423	-5.023	1.00	17.02
ATOM	1941	CB	LEU	263	-17.233	-5.281	-2.027	1.00	14.57
ATOM	1942	CG	LEU	263	-16.264	-4.205	-1.525	1.00	19.15
ATOM	1943	CD1	LEU	263	-16.837	-2.811	-1.731	1.00	18.55
ATOM	1944	CD2	LEU	263	-15.965	-4.450	-0.058	1.00	22.85
ATOM	1945	N	GLU	264	-15.344	-6.412	-4.083	1.00	17.48
ATOM	1946	CA	GLU	264	-14.020	-6.530	-4.686	1.00	17.94
ATOM	1947	C	GLU	264	-14.049	-6.405	-6.205	1.00	23.91
ATOM	1948	O	GLU	264	-13.098	-5.912	-6.819	1.00	23.40
ATOM	1949	CB	GLU	264	-13.399	-7.868	-4.306	1.00	18.87
ATOM	1950	CG	GLU	264	-13.258	-8.104	-2.833	1.00	19.89
ATOM	1951	CD	GLU	264	-12.550	-9.399	-2.532	1.00	37.72
ATOM	1952	OE1	GLU	264	-12.828	-10.410	-3.201	1.00	44.58
ATOM	1953	OE2	GLU	264	-11.721	-9.410	-1.603	1.00	30.00
ATOM	1954	N	ASN	265	-15.137	-6.882	-6.797	1.00	22.09
ATOM	1955	CA	ASN	265	-15.314	-6.849	-8.239	1.00	22.25
ATOM	1956	C	ASN	265	-15.950	-5.561	-8.753	1.00	27.73
ATOM	1957	O	ASN	265	-15.660	-5.140	-9.869	1.00	29.41
ATOM	1958	CB	ASN	265	-16.130	-8.060	-8.687	1.00	22.20
ATOM	1959	CG	ASN	265	-15.444	-9.370	-8.354	1.00	53.15
ATOM	1960	OD1	ASN	265	-14.220	-9.492	-8.455	1.00	57.34
ATOM	1961	ND2	ASN	265	-16.222	-10.355	-7.945	1.00	43.73
ATOM	1962	N	GLU	266	-16.765	-4.909	-7.925	1.00	23.88
ATOM	1963	CA	GLU	266	-17.443	-3.671	-8.319	1.00	22.90
ATOM	1964	C	GLU	266	-16.629	-2.405	-8.094	1.00	22.66
ATOM	1965	O	GLU	266	-16.998	-1.341	-8.582	1.00	22.09

ATOM	1966	CB	GLU	266	-18.799	-3.528	-7.612	1.00	24.33
ATOM	1967	CG	GLU	266	-19.788	-4.625	-7.915	1.00	33.86
ATOM	1968	CD	GLU	266	-19.966	-4.898	-9.389	1.00	49.63
ATOM	1969	OE1	GLU	266	-19.961	-3.949	-10.197	1.00	53.44
ATOM	1970	OE2	GLU	266	-20.118	-6.089	-9.730	1.00	40.15
ATOM	1971	N	LEU	267	-15.540	-2.510	-7.344	1.00	17.14
ATOM	1972	CA	LEU	267	-14.677	-1.363	-7.071	1.00	16.91
ATOM	1973	C	LEU	267	-14.142	-0.753	-8.354	1.00	17.74
ATOM	1974	O	LEU	267	-13.696	-1.476	-9.237	1.00	17.47
ATOM	1975	CB	LEU	267	-13.502	-1.792	-6.175	1.00	17.63
ATOM	1976	CG	LEU	267	-13.838	-2.150	-4.711	1.00	21.24
ATOM	1977	CD1	LEU	267	-12.623	-2.724	-4.006	1.00	19.84
ATOM	1978	CD2	LEU	267	-14.367	-0.924	-3.974	1.00	22.52
ATOM	1979	N	THR	268	-14.178	0.574	-8.448	1.00	13.80
ATOM	1980	CA	THR	268	-13.693	1.278	-9.640	1.00	14.54
ATOM	1981	C	THR	268	-13.074	2.610	-9.214	1.00	18.77
ATOM	1982	O	THR	268	-13.603	3.273	-8.326	1.00	19.12
ATOM	1983	CB	THR	268	-14.849	1.596	-10.641	1.00	25.88
ATOM	1984	OG1	THR	268	-15.647	2.688	-10.150	1.00	29.63
ATOM	1985	CG2	THR	268	-15.740	0.391	-10.844	1.00	23.81
ATOM	1986	N	HIS	269	-11.998	3.031	-9.876	1.00	16.16
ATOM	1987	CA	HIS	269	-11.353	4.297	-9.525	1.00	17.99
ATOM	1988	C	HIS	269	-12.393	5.422	-9.484	1.00	28.56
ATOM	1989	O	HIS	269	-12.331	6.298	-8.617	1.00	29.22
ATOM	1990	CB	HIS	269	-10.222	4.639	-10.512	1.00	18.15
ATOM	1991	CG	HIS	269	-9.671	6.032	-10.359	1.00	21.26
ATOM	1992	ND1	HIS	269	-9.487	6.873	-11.437	1.00	23.32
ATOM	1993	CD2	HIS	269	-9.255	6.718	-9.273	1.00	23.72
ATOM	1994	CE1	HIS	269	-8.978	8.019	-11.021	1.00	23.01
ATOM	1995	NE2	HIS	269	-8.827	7.954	-9.712	1.00	23.46
ATOM	1996	N	ASP	270	-13.376	5.334	-10.378	1.00	27.36
ATOM	1997	CA	ASP	270	-14.452	6.318	-10.471	1.00	28.28
ATOM	1998	C	ASP	270	-15.204	6.391	-9.148	1.00	29.01
ATOM	1999	O	ASP	270	-15.198	7.424	-8.484	1.00	28.48
ATOM	2000	CB	ASP	270	-15.415	5.934	-11.614	1.00	31.89
ATOM	2001	CG	ASP	270	-16.509	6.984	-11.879	1.00	57.52
ATOM	2002	OD1	ASP	270	-16.777	7.870	-11.039	1.00	60.70
ATOM	2003	OD2	ASP	270	-17.125	6.907	-12.967	1.00	66.96
ATOM	2004	N	ILE	271	-15.783	5.263	-8.748	1.00	23.52
ATOM	2005	CA	ILE	271	-16.561	5.147	-7.513	1.00	22.65
ATOM	2006	C	ILE	271	-15.771	5.628	-6.300	1.00	22.26
ATOM	2007	O	ILE	271	-16.306	6.309	-5.427	1.00	23.05
ATOM	2008	CB	ILE	271	-17.015	3.682	-7.279	1.00	26.80
ATOM	2009	CG1	ILE	271	-17.922	3.220	-8.419	1.00	28.03
ATOM	2010	CG2	ILE	271	-17.769	3.546	-5.986	1.00	28.26
ATOM	2011	CD1	ILE	271	-18.340	1.771	-8.315	1.00	35.59
ATOM	2012	N	ILE	272	-14.479	5.327	-6.280	1.00	15.32
ATOM	2013	CA	ILE	272	-13.629	5.723	-5.169	1.00	13.20
ATOM	2014	C	ILE	272	-13.386	7.220	-5.194	1.00	19.00
ATOM	2015	O	ILE	272	-13.359	7.867	-4.144	1.00	19.72
ATOM	2016	CB	ILE	272	-12.333	4.890	-5.127	1.00	14.50
ATOM	2017	CG1	ILE	272	-12.697	3.447	-4.740	1.00	13.26
ATOM	2018	CG2	ILE	272	-11.356	5.477	-4.127	1.00	14.10
ATOM	2019	CD1	ILE	272	-11.552	2.478	-4.761	1.00	24.26

ATOM	2020	N	THR	273	-13.293	7.785	-6.391	1.00	18.09
ATOM	2021	CA	THR	273	-13.097	9.230	-6.518	1.00	19.45
ATOM	2022	C	THR	273	-14.405	9.895	-6.078	1.00	26.47
ATOM	2023	O	THR	273	-14.402	10.942	-5.439	1.00	26.83
ATOM	2024	CB	THR	273	-12.760	9.650	-7.973	1.00	23.14
ATOM	2025	OG1	THR	273	-11.562	8.984	-8.398	1.00	24.17
ATOM	2026	CG2	THR	273	-12.557	11.157	-8.064	1.00	16.16
ATOM	2027	N	LYS	274	-15.515	9.217	-6.342	1.00	24.49
ATOM	2028	CA	LYS	274	-16.835	9.707	-5.975	1.00	24.48
ATOM	2029	C	LYS	274	-16.877	9.833	-4.447	1.00	30.41
ATOM	2030	O	LYS	274	-17.290	10.858	-3.907	1.00	32.51
ATOM	2031	CB	LYS	274	-17.880	8.712	-6.462	1.00	26.15
ATOM	2032	CG	LYS	274	-19.293	9.228	-6.588	1.00	50.14
ATOM	2033	CD	LYS	274	-20.187	8.156	-7.193	1.00	66.22
ATOM	2034	CE	LYS	274	-19.701	7.754	-8.580	1.00	82.49
ATOM	2035	NZ	LYS	274	-20.447	6.600	-9.135	1.00	95.34
ATOM	2036	N	PHE	275	-16.370	8.817	-3.759	1.00	23.58
ATOM	2037	CA	PHE	275	-16.346	8.831	-2.306	1.00	21.54
ATOM	2038	C	PHE	275	-15.431	9.927	-1.801	1.00	21.45
ATOM	2039	O	PHE	275	-15.793	10.659	-0.898	1.00	21.56
ATOM	2040	CB	PHE	275	-15.907	7.471	-1.749	1.00	23.59
ATOM	2041	CG	PHE	275	-16.911	6.369	-1.974	1.00	24.46
ATOM	2042	CD1	PHE	275	-18.236	6.520	-1.561	1.00	26.80
ATOM	2043	CD2	PHE	275	-16.547	5.197	-2.609	1.00	26.12
ATOM	2044	CE1	PHE	275	-19.176	5.523	-1.778	1.00	26.69
ATOM	2045	CE2	PHE	275	-17.488	4.196	-2.828	1.00	29.22
ATOM	2046	CZ	PHE	275	-18.805	4.364	-2.412	1.00	26.65
ATOM	2047	N	LEU	276	-14.258	10.062	-2.414	1.00	16.44
ATOM	2048	CA	LEU	276	-13.300	11.086	-2.000	1.00	15.37
ATOM	2049	C	LEU	276	-13.894	12.484	-2.078	1.00	24.02
ATOM	2050	O	LEU	276	-13.819	13.255	-1.123	1.00	25.62
ATOM	2051	CB	LEU	276	-12.030	11.019	-2.839	1.00	14.37
ATOM	2052	CG	LEU	276	-11.187	9.776	-2.553	1.00	19.14
ATOM	2053	CD1	LEU	276	-9.889	9.868	-3.336	1.00	19.35
ATOM	2054	CD2	LEU	276	-10.887	9.649	-1.054	1.00	22.14
ATOM	2055	N	GLU	277	-14.539	12.781	-3.200	1.00	22.07
ATOM	2056	CA	GLU	277	-15.162	14.077	-3.400	1.00	22.27
ATOM	2057	C	GLU	277	-16.323	14.256	-2.425	1.00	30.33
ATOM	2058	O	GLU	277	-16.852	15.359	-2.275	1.00	34.24
ATOM	2059	CB	GLU	277	-15.651	14.231	-4.848	1.00	23.70
ATOM	2060	CG	GLU	277	-14.592	13.986	-5.934	1.00	37.77
ATOM	2061	CD	GLU	277	-13.401	14.944	-5.905	1.00	65.64
ATOM	2062	OE1	GLU	277	-13.273	15.769	-4.976	1.00	72.39
ATOM	2063	OE2	GLU	277	-12.577	14.856	-6.836	1.00	57.27
ATOM	2064	N	ASN	278	-16.705	13.176	-1.747	1.00	24.83
ATOM	2065	CA	ASN	278	-17.788	13.226	-0.774	1.00	23.02
ATOM	2066	C	ASN	278	-17.337	13.798	0.553	1.00	23.90
ATOM	2067	O	ASN	278	-16.453	13.251	1.210	1.00	20.54
ATOM	2068	CB	ASN	278	-18.421	11.851	-0.537	1.00	24.64
ATOM	2069	CG	ASN	278	-19.519	11.899	0.505	1.00	63.15
ATOM	2070	OD1	ASN	278	-19.716	10.950	1.262	1.00	59.86
ATOM	2071	ND2	ASN	278	-20.240	13.018	0.556	1.00	61.71
ATOM	2072	N	GLU	279	-17.974	14.903	0.940	1.00	23.66
ATOM	2073	CA	GLU	279	-17.664	15.588	2.192	1.00	24.15

ATOM	2074	C	GLU	279	-18.810	15.596	3.209	1.00	28.94
ATOM	2075	O	GLU	279	-18.790	16.360	4.163	1.00	29.34
ATOM	2076	CB	GLU	279	-17.185	17.004	1.905	1.00	25.78
ATOM	2077	CG	GLU	279	-15.827	17.082	1.214	1.00	44.13
ATOM	2078	CD	GLU	279	-15.420	18.506	0.860	1.00	92.58
ATOM	2079	OE1	GLU	279	-15.927	19.466	1.482	1.00	100.65
ATOM	2080	OE2	GLU	279	-14.574	18.664	-0.042	1.00	100.57
ATOM	2081	N	ASP	280	-19.791	14.717	3.016	1.00	23.99
ATOM	2082	CA	ASP	280	-20.933	14.607	3.920	1.00	22.02
ATOM	2083	C	ASP	280	-20.564	13.769	5.137	1.00	22.41
ATOM	2084	O	ASP	280	-19.554	13.071	5.138	1.00	22.95
ATOM	2085	CB	ASP	280	-22.108	13.957	3.209	1.00	24.35
ATOM	2086	CG	ASP	280	-22.693	14.833	2.151	1.00	42.62
ATOM	2087	OD1	ASP	280	-23.039	15.985	2.456	1.00	45.44
ATOM	2088	OD2	ASP	280	-22.818	14.362	0.998	1.00	52.57
ATOM	2089	N	ARG	281	-21.420	13.871	6.172	1.00	14.63
ATOM	2090	CA	ARG	281	-21.201	13.094	7.380	1.00	11.86
ATOM	2091	C	ARG	281	-22.517	12.866	8.067	1.00	15.11
ATOM	2092	O	ARG	281	-23.465	13.601	7.840	1.00	15.94
ATOM	2093	CB	ARG	281	-20.312	13.857	8.381	1.00	10.33
ATOM	2094	CG	ARG	281	-18.855	13.944	7.893	1.00	19.95
ATOM	2095	CD	ARG	281	-18.034	14.659	8.979	1.00	9.99
ATOM	2096	NE	ARG	281	-16.672	14.863	8.523	1.00	12.05
ATOM	2097	CZ	ARG	281	-15.699	14.096	8.926	1.00	20.69
ATOM	2098	NH1	ARG	281	-15.913	13.105	9.741	1.00	1.00
ATOM	2099	NH2	ARG	281	-14.491	14.329	8.503	1.00	29.15
ATOM	2100	N	ARG	282	-22.567	11.832	8.927	1.00	10.27
ATOM	2101	CA	ARG	282	-23.782	11.605	9.690	1.00	9.47
ATOM	2102	C	ARG	282	-23.459	10.913	10.984	1.00	16.55
ATOM	2103	O	ARG	282	-22.391	10.338	11.117	1.00	17.04
ATOM	2104	CB	ARG	282	-24.841	10.828	8.881	1.00	3.07
ATOM	2105	CG	ARG	282	-24.354	9.403	8.551	1.00	5.84
ATOM	2106	CD	ARG	282	-25.536	8.601	7.978	1.00	25.67
ATOM	2107	NE	ARG	282	-25.077	7.326	7.458	1.00	38.49
ATOM	2108	CZ	ARG	282	-25.151	7.044	6.188	1.00	48.45
ATOM	2109	NH1	ARG	282	-25.622	7.902	5.330	1.00	26.72
ATOM	2110	NH2	ARG	282	-24.745	5.883	5.771	1.00	34.81
ATOM	2111	N	SER	283	-24.392	10.980	11.953	1.00	12.72
ATOM	2112	CA	SER	283	-24.123	10.333	13.224	1.00	11.68
ATOM	2113	C	SER	283	-24.128	8.839	13.064	1.00	12.67
ATOM	2114	O	SER	283	-24.929	8.308	12.313	1.00	12.85
ATOM	2115	CB	SER	283	-25.111	10.784	14.317	1.00	17.91
ATOM	2116	OG	SER	283	-26.441	10.375	13.989	1.00	28.36
ATOM	2117	N	ALA	284	-23.205	8.167	13.778	1.00	8.25
ATOM	2118	CA	ALA	284	-23.139	6.721	13.670	1.00	7.48
ATOM	2119	C	ALA	284	-22.279	6.151	14.763	1.00	10.55
ATOM	2120	O	ALA	284	-21.442	6.846	15.319	1.00	7.46
ATOM	2121	CB	ALA	284	-22.601	6.288	12.293	1.00	8.05
ATOM	2122	N	SER	285	-22.513	4.860	15.071	1.00	8.44
ATOM	2123	CA	SER	285	-21.746	4.231	16.131	1.00	10.17
ATOM	2124	C	SER	285	-20.691	3.352	15.519	1.00	16.06
ATOM	2125	O	SER	285	-20.897	2.161	15.337	1.00	19.28
ATOM	2126	CB	SER	285	-22.719	3.436	17.021	1.00	17.06
ATOM	2127	OG	SER	285	-23.635	4.344	17.641	1.00	34.64

ATOM	2128	N	LEU	286	-19.539	3.969	15.197	1.00	8.68
ATOM	2129	CA	LEU	286	-18.495	3.216	14.531	1.00	7.51
ATOM	2130	C	LEU	286	-17.713	2.313	15.464	1.00	13.65
ATOM	2131	O	LEU	286	-17.269	2.749	16.535	1.00	14.46
ATOM	2132	CB	LEU	286	-17.510	4.166	13.833	1.00	7.11
ATOM	2133	CG	LEU	286	-16.310	3.517	13.130	1.00	10.35
ATOM	2134	CD1	LEU	286	-16.783	2.793	11.883	1.00	10.07
ATOM	2135	CD2	LEU	286	-15.277	4.552	12.771	1.00	10.77
ATOM	2136	N	HIS	287	-17.564	1.052	15.060	1.00	10.80
ATOM	2137	CA	HIS	287	-16.767	0.068	15.801	1.00	12.55
ATOM	2138	C	HIS	287	-15.702	-0.357	14.803	1.00	13.43
ATOM	2139	O	HIS	287	-15.989	-1.099	13.871	1.00	14.75
ATOM	2140	CB	HIS	287	-17.580	-1.170	16.170	1.00	14.98
ATOM	2141	CG	HIS	287	-18.581	-0.946	17.257	1.00	19.45
ATOM	2142	ND1	HIS	287	-19.745	-0.235	17.064	1.00	21.98
ATOM	2143	CD2	HIS	287	-18.618	-1.394	18.531	1.00	21.47
ATOM	2144	CE1	HIS	287	-20.462	-0.253	18.172	1.00	21.49
ATOM	2145	NE2	HIS	287	-19.796	-0.953	19.078	1.00	21.79
ATOM	2146	N	LEU	288	-14.479	0.104	15.000	1.00	4.50
ATOM	2147	CA	LEU	288	-13.391	-0.230	14.099	1.00	2.17
ATOM	2148	C	LEU	288	-12.321	-0.947	14.904	1.00	11.97
ATOM	2149	O	LEU	288	-11.891	-0.449	15.943	1.00	12.25
ATOM	2150	CB	LEU	288	-12.841	1.046	13.467	1.00	1.00
ATOM	2151	CG	LEU	288	-11.665	0.921	12.504	1.00	3.34
ATOM	2152	CD1	LEU	288	-12.073	0.170	11.231	1.00	2.56
ATOM	2153	CD2	LEU	288	-11.163	2.312	12.180	1.00	2.67
ATOM	2154	N	PRO	289	-11.911	-2.150	14.469	1.00	13.97
ATOM	2155	CA	PRO	289	-10.883	-2.892	15.200	1.00	15.61
ATOM	2156	C	PRO	289	-9.483	-2.272	15.154	1.00	22.55
ATOM	2157	O	PRO	289	-9.046	-1.715	14.140	1.00	22.15
ATOM	2158	CB	PRO	289	-10.889	-4.257	14.506	1.00	17.38
ATOM	2159	CG	PRO	289	-11.304	-3.925	13.106	1.00	21.04
ATOM	2160	CD	PRO	289	-12.422	-2.953	13.338	1.00	15.79
ATOM	2161	N	LYS	290	-8.779	-2.419	16.262	1.00	19.44
ATOM	2162	CA	LYS	290	-7.421	-1.945	16.392	1.00	18.93
ATOM	2163	C	LYS	290	-6.631	-3.126	15.838	1.00	24.83
ATOM	2164	O	LYS	290	-6.953	-4.279	16.151	1.00	25.89
ATOM	2165	CB	LYS	290	-7.123	-1.718	17.874	1.00	20.28
ATOM	2166	CG	LYS	290	-5.749	-1.192	18.216	1.00	35.38
ATOM	2167	CD	LYS	290	-5.683	-0.954	19.701	1.00	53.02
ATOM	2168	CE	LYS	290	-4.319	-0.512	20.181	1.00	77.66
ATOM	2169	NZ	LYS	290	-4.355	-0.183	21.634	1.00	94.71
ATOM	2170	N	LEU	291	-5.663	-2.859	14.963	1.00	22.36
ATOM	2171	CA	LEU	291	-4.862	-3.928	14.375	1.00	22.32
ATOM	2172	C	LEU	291	-3.587	-3.451	13.708	1.00	25.74
ATOM	2173	O	LEU	291	-3.507	-2.315	13.271	1.00	26.04
ATOM	2174	CB	LEU	291	-5.695	-4.711	13.356	1.00	22.24
ATOM	2175	CG	LEU	291	-5.983	-4.114	11.974	1.00	26.16
ATOM	2176	CD1	LEU	291	-6.823	-5.127	11.218	1.00	26.63
ATOM	2177	CD2	LEU	291	-6.688	-2.778	12.043	1.00	28.41
ATOM	2178	N	SER	292	-2.600	-4.335	13.619	1.00	21.54
ATOM	2179	CA	SER	292	-1.343	-4.005	12.973	1.00	22.64
ATOM	2180	C	SER	292	-1.020	-5.132	11.999	1.00	29.52
ATOM	2181	O	SER	292	-0.215	-6.017	12.310	1.00	31.69

ATOM	2182	CB	SER	292	-0.242	-3.869	14.011	1.00	27.63
ATOM	2183	OG	SER	292	-0.234	-5.017	14.832	1.00	48.56
ATOM	2184	N	ILE	293	-1.655	-5.102	10.827	1.00	23.99
ATOM	2185	CA	ILE	293	-1.450	-6.142	9.828	1.00	21.90
ATOM	2186	C	ILE	293	-0.240	-5.896	8.939	1.00	19.80
ATOM	2187	O	ILE	293	0.239	-4.765	8.807	1.00	16.63
ATOM	2188	CB	ILE	293	-2.721	-6.377	8.961	1.00	24.75
ATOM	2189	CG1	ILE	293	-3.077	-5.118	8.167	1.00	22.26
ATOM	2190	CG2	ILE	293	-3.881	-6.807	9.851	1.00	27.40
ATOM	2191	CD1	ILE	293	-4.156	-5.351	7.138	1.00	4.10
ATOM	2192	N	THR	294	0.207	-6.963	8.288	1.00	14.89
ATOM	2193	CA	THR	294	1.360	-6.896	7.416	1.00	14.93
ATOM	2194	C	THR	294	1.078	-7.602	6.098	1.00	19.13
ATOM	2195	O	THR	294	0.112	-8.354	5.977	1.00	18.47
ATOM	2196	CB	THR	294	2.572	-7.552	8.089	1.00	28.48
ATOM	2197	OG1	THR	294	2.622	-7.140	9.462	1.00	35.90
ATOM	2198	CG2	THR	294	3.857	-7.128	7.405	1.00	30.05
ATOM	2199	N	GLY	295	1.900	-7.312	5.099	1.00	16.51
ATOM	2200	CA	GLY	295	1.749	-7.936	3.805	1.00	16.34
ATOM	2201	C	GLY	295	3.122	-8.117	3.200	1.00	19.13
ATOM	2202	O	GLY	295	3.769	-7.137	2.822	1.00	20.78
ATOM	2203	N	THR	296	3.607	-9.354	3.189	1.00	11.65
ATOM	2204	CA	THR	296	4.909	-9.646	2.618	1.00	10.24
ATOM	2205	C	THR	296	4.626	-10.381	1.319	1.00	15.86
ATOM	2206	O	THR	296	3.856	-11.346	1.293	1.00	17.65
ATOM	2207	CB	THR	296	5.772	-10.506	3.557	1.00	13.92
ATOM	2208	OG1	THR	296	5.654	-10.015	4.899	1.00	20.85
ATOM	2209	CG2	THR	296	7.223	-10.411	3.153	1.00	6.06
ATOM	2210	N	TYR	297	5.213	-9.884	0.235	1.00	11.45
ATOM	2211	CA	TYR	297	5.005	-10.441	-1.089	1.00	10.22
ATOM	2212	C	TYR	297	6.292	-10.521	-1.897	1.00	12.07
ATOM	2213	O	TYR	297	7.174	-9.691	-1.737	1.00	10.00
ATOM	2214	CB	TYR	297	4.014	-9.562	-1.871	1.00	10.72
ATOM	2215	CG	TYR	297	2.669	-9.442	-1.207	1.00	10.66
ATOM	2216	CD1	TYR	297	1.758	-10.487	-1.259	1.00	11.37
ATOM	2217	CD2	TYR	297	2.332	-8.315	-0.460	1.00	12.31
ATOM	2218	CE1	TYR	297	0.546	-10.416	-0.576	1.00	12.44
ATOM	2219	CE2	TYR	297	1.125	-8.243	0.225	1.00	13.17
ATOM	2220	CZ	TYR	297	0.236	-9.301	0.165	1.00	19.37
ATOM	2221	OH	TYR	297	-0.956	-9.274	0.854	1.00	21.32
ATOM	2222	N	ASP	298	6.347	-11.523	-2.780	1.00	8.38
ATOM	2223	CA	ASP	298	7.443	-11.777	-3.721	1.00	7.18
ATOM	2224	C	ASP	298	7.002	-11.149	-5.042	1.00	15.56
ATOM	2225	O	ASP	298	6.188	-11.728	-5.777	1.00	17.52
ATOM	2226	CB	ASP	298	7.614	-13.286	-3.923	1.00	8.20
ATOM	2227	CG	ASP	298	8.677	-13.647	-4.958	1.00	13.40
ATOM	2228	OD1	ASP	298	9.392	-12.771	-5.468	1.00	12.72
ATOM	2229	OD2	ASP	298	8.800	-14.855	-5.259	1.00	19.52
ATOM	2230	N	LEU	299	7.546	-9.975	-5.334	1.00	10.89
ATOM	2231	CA	LEU	299	7.209	-9.228	-6.539	1.00	7.89
ATOM	2232	C	LEU	299	7.509	-9.976	-7.813	1.00	8.02
ATOM	2233	O	LEU	299	6.818	-9.799	-8.807	1.00	6.03
ATOM	2234	CB	LEU	299	7.909	-7.871	-6.553	1.00	7.31
ATOM	2235	CG	LEU	299	7.540	-6.923	-5.408	1.00	10.69

ATOM	2236	CD1	LEU	299	8.295	-5.624	-5.553	1.00	9.61
ATOM	2237	CD2	LEU	299	6.031	-6.681	-5.396	1.00	12.99
ATOM	2238	N	LYS	300	8.534	-10.816	-7.778	1.00	5.30
ATOM	2239	CA	LYS	300	8.903	-11.599	-8.948	1.00	6.84
ATOM	2240	C	LYS	300	7.714	-12.453	-9.355	1.00	14.89
ATOM	2241	O	LYS	300	7.308	-12.472	-10.518	1.00	15.15
ATOM	2242	CB	LYS	300	10.091	-12.495	-8.624	1.00	9.49
ATOM	2243	CG	LYS	300	10.488	-13.488	-9.710	1.00	27.80
ATOM	2244	CD	LYS	300	11.752	-14.226	-9.292	1.00	44.37
ATOM	2245	CE	LYS	300	12.067	-15.433	-10.159	1.00	56.70
ATOM	2246	NZ	LYS	300	13.235	-16.166	-9.598	1.00	65.57
ATOM	2247	N	SER	301	7.126	-13.101	-8.359	1.00	12.97
ATOM	2248	CA	SER	301	5.968	-13.955	-8.553	1.00	13.55
ATOM	2249	C	SER	301	4.730	-13.125	-8.866	1.00	20.42
ATOM	2250	O	SER	301	4.186	-13.198	-9.976	1.00	21.11
ATOM	2251	CB	SER	301	5.715	-14.775	-7.290	1.00	16.92
ATOM	2252	OG	SER	301	4.473	-15.458	-7.351	1.00	27.19
ATOM	2253	N	VAL	302	4.330	-12.294	-7.901	1.00	16.40
ATOM	2254	CA	VAL	302	3.141	-11.466	-8.031	1.00	15.66
ATOM	2255	C	VAL	302	3.096	-10.612	-9.303	1.00	20.29
ATOM	2256	O	VAL	302	2.143	-10.734	-10.071	1.00	22.41
ATOM	2257	CB	VAL	302	2.875	-10.648	-6.736	1.00	19.18
ATOM	2258	CG1	VAL	302	3.876	-9.559	-6.548	1.00	19.85
ATOM	2259	CG2	VAL	302	1.485	-10.106	-6.741	1.00	18.82
ATOM	2260	N	LEU	303	4.145	-9.839	-9.579	1.00	15.73
ATOM	2261	CA	LEU	303	4.192	-8.994	-10.777	1.00	15.23
ATOM	2262	C	LEU	303	4.363	-9.818	-12.048	1.00	20.33
ATOM	2263	O	LEU	303	3.923	-9.409	-13.121	1.00	21.23
ATOM	2264	CB	LEU	303	5.316	-7.959	-10.679	1.00	14.99
ATOM	2265	CG	LEU	303	5.243	-6.859	-9.616	1.00	18.53
ATOM	2266	CD1	LEU	303	6.568	-6.176	-9.539	1.00	17.77
ATOM	2267	CD2	LEU	303	4.150	-5.869	-9.915	1.00	21.75
ATOM	2268	N	GLY	304	4.988	-10.982	-11.923	1.00	17.32
ATOM	2269	CA	GLY	304	5.185	-11.847	-13.072	1.00	17.32
ATOM	2270	C	GLY	304	3.822	-12.252	-13.578	1.00	20.79
ATOM	2271	O	GLY	304	3.581	-12.367	-14.774	1.00	21.89
ATOM	2272	N	GLN	305	2.907	-12.413	-12.636	1.00	14.97
ATOM	2273	CA	GLN	305	1.532	-12.767	-12.931	1.00	14.25
ATOM	2274	C	GLN	305	0.895	-11.600	-13.688	1.00	22.05
ATOM	2275	O	GLN	305	-0.039	-11.779	-14.467	1.00	26.91
ATOM	2276	CB	GLN	305	0.778	-12.974	-11.625	1.00	14.88
ATOM	2277	CG	GLN	305	1.327	-14.084	-10.715	1.00	18.29
ATOM	2278	CD	GLN	305	0.725	-15.437	-11.007	1.00	41.01
ATOM	2279	OE1	GLN	305	-0.496	-15.582	-11.109	1.00	35.49
ATOM	2280	NE2	GLN	305	1.574	-16.445	-11.128	1.00	40.19
ATOM	2281	N	LEU	306	1.377	-10.393	-13.423	1.00	16.39
ATOM	2282	CA	LEU	306	0.865	-9.209	-14.096	1.00	15.33
ATOM	2283	C	LEU	306	1.569	-9.023	-15.439	1.00	21.51
ATOM	2284	O	LEU	306	1.346	-8.028	-16.130	1.00	20.80
ATOM	2285	CB	LEU	306	1.070	-7.974	-13.222	1.00	14.47
ATOM	2286	CG	LEU	306	0.133	-7.906	-12.017	1.00	17.83
ATOM	2287	CD1	LEU	306	0.536	-6.803	-11.065	1.00	18.30
ATOM	2288	CD2	LEU	306	-1.273	-7.702	-12.492	1.00	20.75
ATOM	2289	N	GLY	307	2.425	-9.977	-15.797	1.00	19.62

ATOM	2290	CA	GLY	307	3.138	-9.908	-17.060	1.00	19.49
ATOM	2291	C	GLY	307	4.564	-9.387	-17.023	1.00	22.62
ATOM	2292	O	GLY	307	5.229	-9.365	-18.058	1.00	24.17
ATOM	2293	N	ILE	308	5.039	-8.942	-15.864	1.00	15.79
ATOM	2294	CA	ILE	308	6.416	-8.434	-15.747	1.00	13.45
ATOM	2295	C	ILE	308	7.337	-9.636	-15.472	1.00	17.26
ATOM	2296	O	ILE	308	7.457	-10.073	-14.328	1.00	18.58
ATOM	2297	CB	ILE	308	6.526	-7.372	-14.612	1.00	14.02
ATOM	2298	CG1	ILE	308	5.560	-6.208	-14.903	1.00	13.26
ATOM	2299	CG2	ILE	308	7.960	-6.888	-14.480	1.00	12.07
ATOM	2300	CD1	ILE	308	5.541	-5.105	-13.864	1.00	10.43
ATOM	2301	N	THR	309	7.956	-10.178	-16.525	1.00	8.26
ATOM	2302	CA	THR	309	8.811	-11.360	-16.386	1.00	6.52
ATOM	2303	C	THR	309	10.231	-11.272	-16.930	1.00	13.71
ATOM	2304	O	THR	309	11.161	-11.895	-16.398	1.00	11.32
ATOM	2305	CB	THR	309	8.169	-12.575	-17.069	1.00	6.64
ATOM	2306	OG1	THR	309	7.898	-12.255	-18.436	1.00	11.86
ATOM	2307	CG2	THR	309	6.883	-12.969	-16.380	1.00	9.03
ATOM	2308	N	LYS	310	10.383	-10.543	-18.025	1.00	15.00
ATOM	2309	CA	LYS	310	11.672	-10.407	-18.684	1.00	16.39
ATOM	2310	C	LYS	310	12.790	-9.798	-17.837	1.00	19.67
ATOM	2311	O	LYS	310	13.943	-10.207	-17.952	1.00	20.38
ATOM	2312	CB	LYS	310	11.502	-9.675	-20.017	1.00	19.91
ATOM	2313	CG	LYS	310	12.456	-10.146	-21.091	1.00	44.14
ATOM	2314	CD	LYS	310	12.119	-9.527	-22.433	1.00	66.75
ATOM	2315	CE	LYS	310	13.082	-9.987	-23.519	1.00	92.02
ATOM	2316	NZ	LYS	310	12.648	-9.534	-24.866	1.00	107.67
ATOM	2317	N	VAL	311	12.444	-8.869	-16.955	1.00	15.16
ATOM	2318	CA	VAL	311	13.441	-8.219	-16.101	1.00	14.87
ATOM	2319	C	VAL	311	14.000	-9.193	-15.066	1.00	19.98
ATOM	2320	O	VAL	311	15.159	-9.079	-14.664	1.00	20.15
ATOM	2321	CB	VAL	311	12.847	-7.020	-15.335	1.00	19.22
ATOM	2322	CG1	VAL	311	13.953	-6.151	-14.768	1.00	18.83
ATOM	2323	CG2	VAL	311	11.963	-6.204	-16.239	1.00	20.20
ATOM	2324	N	PHE	312	13.180	-10.166	-14.671	1.00	16.07
ATOM	2325	CA	PHE	312	13.561	-11.143	-13.661	1.00	15.77
ATOM	2326	C	PHE	312	14.280	-12.349	-14.221	1.00	24.43
ATOM	2327	O	PHE	312	14.750	-13.207	-13.464	1.00	24.24
ATOM	2328	CB	PHE	312	12.327	-11.619	-12.896	1.00	16.71
ATOM	2329	CG	PHE	312	11.509	-10.513	-12.332	1.00	17.34
ATOM	2330	CD1	PHE	312	11.803	-9.970	-11.087	1.00	19.98
ATOM	2331	CD2	PHE	312	10.467	-9.977	-13.068	1.00	20.96
ATOM	2332	CE1	PHE	312	11.059	-8.898	-10.593	1.00	23.38
ATOM	2333	CE2	PHE	312	9.726	-8.910	-12.577	1.00	22.79
ATOM	2334	CZ	PHE	312	10.022	-8.370	-11.340	1.00	21.30
ATOM	2335	N	SER	313	14.341	-12.437	-15.542	1.00	24.14
ATOM	2336	CA	SER	313	14.992	-13.567	-16.166	1.00	25.73
ATOM	2337	C	SER	313	16.289	-13.221	-16.865	1.00	28.61
ATOM	2338	O	SER	313	16.675	-12.059	-16.970	1.00	28.35
ATOM	2339	CB	SER	313	14.048	-14.267	-17.144	1.00	35.21
ATOM	2340	OG	SER	313	14.600	-15.519	-17.558	1.00	55.19
ATOM	2341	N	ASN	314	16.911	-14.265	-17.399	1.00	25.09
ATOM	2342	CA	ASN	314	18.178	-14.194	-18.101	1.00	25.01
ATOM	2343	C	ASN	314	18.150	-13.269	-19.303	1.00	31.47

ATOM	2344	O	ASN	314	19.201	-12.842	-19.780	1.00	33.42
ATOM	2345	CB	ASN	314	18.589	-15.592	-18.543	1.00	28.10
ATOM	2346	CG	ASN	314	18.354	-16.630	-17.466	1.00	58.16
ATOM	2347	OD1	ASN	314	18.962	-16.588	-16.396	1.00	39.70
ATOM	2348	ND2	ASN	314	17.426	-17.540	-17.723	1.00	60.22
ATOM	2349	N	GLY	315	16.960	-12.986	-19.819	1.00	27.06
ATOM	2350	CA	GLY	315	16.857	-12.099	-20.966	1.00	24.95
ATOM	2351	C	GLY	315	16.710	-10.631	-20.600	1.00	23.06
ATOM	2352	O	GLY	315	16.510	-9.784	-21.472	1.00	23.67
ATOM	2353	N	ALA	316	16.777	-10.325	-19.312	1.00	14.60
ATOM	2354	CA	ALA	316	16.640	-8.953	-18.847	1.00	13.39
ATOM	2355	C	ALA	316	17.547	-7.974	-19.577	1.00	15.37
ATOM	2356	O	ALA	316	18.752	-8.198	-19.694	1.00	15.22
ATOM	2357	CB	ALA	316	16.894	-8.889	-17.352	1.00	14.28
ATOM	2358	N	ASP	317	16.970	-6.914	-20.127	1.00	12.56
ATOM	2359	CA	ASP	317	17.766	-5.902	-20.802	1.00	12.70
ATOM	2360	C	ASP	317	17.896	-4.735	-19.834	1.00	17.05
ATOM	2361	O	ASP	317	17.090	-3.800	-19.858	1.00	18.01
ATOM	2362	CB	ASP	317	17.103	-5.444	-22.102	1.00	14.59
ATOM	2363	CG	ASP	317	17.990	-4.512	-22.930	1.00	29.21
ATOM	2364	OD1	ASP	317	18.888	-3.855	-22.359	1.00	27.11
ATOM	2365	OD2	ASP	317	17.785	-4.424	-24.155	1.00	33.52
ATOM	2366	N	LEU	318	18.904	-4.829	-18.964	1.00	12.04
ATOM	2367	CA	LEU	318	19.186	-3.826	-17.945	1.00	10.18
ATOM	2368	C	LEU	318	20.465	-3.058	-18.277	1.00	10.94
ATOM	2369	O	LEU	318	21.299	-2.790	-17.414	1.00	6.64
ATOM	2370	CB	LEU	318	19.291	-4.512	-16.577	1.00	10.05
ATOM	2371	CG	LEU	318	18.012	-5.189	-16.071	1.00	13.27
ATOM	2372	CD1	LEU	318	18.236	-5.923	-14.777	1.00	12.27
ATOM	2373	CD2	LEU	318	16.961	-4.156	-15.898	1.00	19.77
ATOM	2374	N	SER	319	20.567	-2.672	-19.543	1.00	12.25
ATOM	2375	CA	SER	319	21.703	-1.933	-20.069	1.00	15.09
ATOM	2376	C	SER	319	21.872	-0.574	-19.407	1.00	22.50
ATOM	2377	O	SER	319	22.978	-0.038	-19.356	1.00	23.85
ATOM	2378	CB	SER	319	21.547	-1.764	-21.574	1.00	21.82
ATOM	2379	OG	SER	319	21.212	-3.005	-22.174	1.00	36.80
ATOM	2380	N	GLY	320	20.772	-0.025	-18.903	1.00	18.63
ATOM	2381	CA	GLY	320	20.825	1.263	-18.238	1.00	18.09
ATOM	2382	C	GLY	320	21.462	1.095	-16.878	1.00	21.72
ATOM	2383	O	GLY	320	22.005	2.041	-16.303	1.00	21.34
ATOM	2384	N	VAL	321	21.390	-0.127	-16.364	1.00	18.37
ATOM	2385	CA	VAL	321	21.953	-0.431	-15.064	1.00	19.72
ATOM	2386	C	VAL	321	23.424	-0.734	-15.247	1.00	29.96
ATOM	2387	O	VAL	321	24.269	-0.051	-14.671	1.00	30.99
ATOM	2388	CB	VAL	321	21.225	-1.618	-14.366	1.00	22.97
ATOM	2389	CG1	VAL	321	21.785	-1.815	-12.978	1.00	22.52
ATOM	2390	CG2	VAL	321	19.716	-1.351	-14.274	1.00	22.80
ATOM	2391	N	THR	322	23.732	-1.727	-16.074	1.00	28.96
ATOM	2392	CA	THR	322	25.117	-2.092	-16.347	1.00	29.46
ATOM	2393	C	THR	322	25.196	-2.459	-17.836	1.00	34.19
ATOM	2394	O	THR	322	24.518	-3.382	-18.305	1.00	34.65
ATOM	2395	CB	THR	322	25.584	-3.251	-15.433	1.00	40.37
ATOM	2396	OG1	THR	322	26.928	-3.597	-15.735	1.00	47.50
ATOM	2397	CG2	THR	322	24.739	-4.516	-15.594	1.00	38.41

ATOM	2398	N	GLU	323	26.027	-1.706	-18.524	1.00	30.88
ATOM	2399	CA	GLU	323	26.175	-1.771	-19.989	1.00	30.91
ATOM	2400	C	GLU	323	26.718	-3.111	-20.537	1.00	32.45
ATOM	2401	O	GLU	323	26.054	-3.792	-21.330	1.00	32.38
ATOM	2402	CB	GLU	323	27.138	-0.681	-20.464	1.00	32.93
ATOM	2403	CG	GLU	323	26.608	0.735	-20.215	1.00	51.42
ATOM	2404	CD	GLU	323	27.592	1.827	-20.640	1.00	87.20
ATOM	2405	OE1	GLU	323	28.662	1.515	-21.289	1.00	93.43
ATOM	2406	OE2	GLU	323	27.352	3.061	-20.349	1.00	85.51
ATOM	2407	N	GLU	324	27.916	-3.475	-20.117	1.00	28.18
ATOM	2408	CA	GLU	324	28.644	-4.630	-20.704	1.00	28.79
ATOM	2409	C	GLU	324	28.255	-6.038	-20.184	1.00	29.89
ATOM	2410	O	GLU	324	28.256	-7.021	-20.939	1.00	31.67
ATOM	2411	CB	GLU	324	30.145	-4.498	-20.449	1.00	31.18
ATOM	2412	CG	GLU	324	30.965	-4.478	-21.742	1.00	49.76
ATOM	2413	CD	GLU	324	30.289	-3.689	-22.866	1.00	82.83
ATOM	2414	OE1	GLU	324	30.090	-2.421	-22.734	1.00	85.65
ATOM	2415	OE2	GLU	324	29.917	-4.290	-23.946	1.00	80.14
ATOM	2416	N	ALA	325	27.923	-6.181	-18.914	1.00	21.34
ATOM	2417	CA	ALA	325	27.685	-7.537	-18.349	1.00	18.64
ATOM	2418	C	ALA	325	26.208	-7.903	-18.150	1.00	20.20
ATOM	2419	O	ALA	325	25.360	-7.029	-17.928	1.00	19.22
ATOM	2420	CB	ALA	325	28.347	-7.658	-16.975	1.00	19.04
ATOM	2421	N	PRO	326	25.866	-9.200	-18.305	1.00	15.12
ATOM	2422	CA	PRO	326	24.483	-9.642	-18.118	1.00	13.67
ATOM	2423	C	PRO	326	24.001	-9.335	-16.704	1.00	18.85
ATOM	2424	O	PRO	326	24.766	-9.447	-15.739	1.00	20.47
ATOM	2425	CB	PRO	326	24.584	-11.155	-18.346	1.00	13.96
ATOM	2426	CG	PRO	326	26.040	-11.478	-18.090	1.00	17.87
ATOM	2427	CD	PRO	326	26.683	-10.329	-18.791	1.00	14.49
ATOM	2428	N	LEU	327	22.724	-8.984	-16.594	1.00	14.79
ATOM	2429	CA	LEU	327	22.111	-8.649	-15.317	1.00	14.65
ATOM	2430	C	LEU	327	20.612	-8.903	-15.383	1.00	23.21
ATOM	2431	O	LEU	327	20.002	-8.752	-16.439	1.00	25.97
ATOM	2432	CB	LEU	327	22.346	-7.176	-14.992	1.00	13.29
ATOM	2433	CG	LEU	327	21.934	-6.704	-13.604	1.00	15.65
ATOM	2434	CD1	LEU	327	22.728	-7.487	-12.608	1.00	16.46
ATOM	2435	CD2	LEU	327	22.180	-5.219	-13.444	1.00	14.83
ATOM	2436	N	LYS	328	20.022	-9.268	-14.248	1.00	15.80
ATOM	2437	CA	LYS	328	18.595	-9.530	-14.166	1.00	12.06
ATOM	2438	C	LYS	328	18.190	-9.361	-12.714	1.00	15.70
ATOM	2439	O	LYS	328	19.034	-9.401	-11.821	1.00	14.81
ATOM	2440	CB	LYS	328	18.287	-10.945	-14.632	1.00	12.41
ATOM	2441	CG	LYS	328	18.745	-12.020	-13.677	1.00	15.34
ATOM	2442	CD	LYS	328	18.376	-13.387	-14.205	1.00	23.38
ATOM	2443	CE	LYS	328	18.873	-14.531	-13.333	1.00	34.78
ATOM	2444	NZ	LYS	328	18.529	-15.847	-13.942	1.00	52.92
ATOM	2445	N	LEU	329	16.893	-9.193	-12.483	1.00	14.22
ATOM	2446	CA	LEU	329	16.362	-8.995	-11.138	1.00	13.57
ATOM	2447	C	LEU	329	16.019	-10.323	-10.475	1.00	18.65
ATOM	2448	O	LEU	329	14.945	-10.884	-10.685	1.00	17.39
ATOM	2449	CB	LEU	329	15.143	-8.079	-11.184	1.00	12.21
ATOM	2450	CG	LEU	329	14.728	-7.426	-9.873	1.00	14.57
ATOM	2451	CD1	LEU	329	15.929	-6.837	-9.172	1.00	13.69

ATOM	2452	CD2	LEU	329	13.705	-6.354	-10.180	1.00	14.70
ATOM	2453	N	SER	330	16.964	-10.809	-9.680	1.00	15.18
ATOM	2454	CA	SER	330	16.847	-12.071	-8.977	1.00	14.75
ATOM	2455	C	SER	330	15.939	-11.963	-7.766	1.00	19.86
ATOM	2456	O	SER	330	15.165	-12.879	-7.482	1.00	22.85
ATOM	2457	CB	SER	330	18.231	-12.532	-8.525	1.00	21.05
ATOM	2458	OG	SER	330	19.203	-12.336	-9.544	1.00	39.22
ATOM	2459	N	LYS	331	16.011	-10.838	-7.067	1.00	13.26
ATOM	2460	CA	LYS	331	15.195	-10.653	-5.880	1.00	11.98
ATOM	2461	C	LYS	331	14.383	-9.353	-5.953	1.00	12.78
ATOM	2462	O	LYS	331	14.894	-8.310	-6.348	1.00	11.98
ATOM	2463	CB	LYS	331	16.094	-10.668	-4.622	1.00	13.85
ATOM	2464	CG	LYS	331	15.424	-11.219	-3.355	1.00	13.58
ATOM	2465	CD	LYS	331	15.211	-12.736	-3.420	1.00	14.30
ATOM	2466	CE	LYS	331	14.024	-13.191	-2.567	1.00	17.75
ATOM	2467	NZ	LYS	331	14.238	-12.980	-1.115	1.00	46.06
ATOM	2468	N	ALA	332	13.095	-9.444	-5.651	1.00	8.06
ATOM	2469	CA	ALA	332	12.222	-8.274	-5.628	1.00	7.65
ATOM	2470	C	ALA	332	11.167	-8.619	-4.572	1.00	11.68
ATOM	2471	O	ALA	332	10.302	-9.471	-4.785	1.00	9.24
ATOM	2472	CB	ALA	332	11.591	-8.033	-6.998	1.00	8.18
ATOM	2473	N	VAL	333	11.309	-8.026	-3.394	1.00	9.58
ATOM	2474	CA	VAL	333	10.394	-8.297	-2.294	1.00	9.85
ATOM	2475	C	VAL	333	9.725	-7.032	-1.758	1.00	13.40
ATOM	2476	O	VAL	333	10.352	-5.973	-1.684	1.00	12.46
ATOM	2477	CB	VAL	333	11.137	-9.022	-1.132	1.00	13.78
ATOM	2478	CG1	VAL	333	10.172	-9.353	0.014	1.00	12.99
ATOM	2479	CG2	VAL	333	11.800	-10.290	-1.645	1.00	13.83
ATOM	2480	N	HIS	334	8.441	-7.152	-1.427	1.00	9.41
ATOM	2481	CA	HIS	334	7.669	-6.060	-0.873	1.00	9.17
ATOM	2482	C	HIS	334	7.117	-6.514	0.469	1.00	15.24
ATOM	2483	O	HIS	334	6.784	-7.688	0.632	1.00	15.50
ATOM	2484	CB	HIS	334	6.493	-5.694	-1.787	1.00	9.35
ATOM	2485	CG	HIS	334	5.638	-4.579	-1.254	1.00	11.86
ATOM	2486	ND1	HIS	334	5.966	-3.245	-1.391	1.00	13.40
ATOM	2487	CD2	HIS	334	4.461	-4.609	-0.593	1.00	12.02
ATOM	2488	CE1	HIS	334	5.025	-2.501	-0.834	1.00	12.10
ATOM	2489	NE2	HIS	334	4.101	-3.309	-0.343	1.00	11.99
ATOM	2490	N	LYS	335	7.064	-5.592	1.427	1.00	12.37
ATOM	2491	CA	LYS	335	6.505	-5.848	2.752	1.00	11.91
ATOM	2492	C	LYS	335	5.866	-4.565	3.239	1.00	15.10
ATOM	2493	O	LYS	335	6.538	-3.542	3.391	1.00	15.49
ATOM	2494	CB	LYS	335	7.562	-6.311	3.756	1.00	15.51
ATOM	2495	CG	LYS	335	6.958	-6.733	5.106	1.00	37.80
ATOM	2496	CD	LYS	335	8.018	-7.241	6.074	1.00	44.20
ATOM	2497	CE	LYS	335	7.448	-7.512	7.445	1.00	53.49
ATOM	2498	NZ	LYS	335	6.509	-8.655	7.395	1.00	71.81
ATOM	2499	N	ALA	336	4.550	-4.598	3.387	1.00	11.02
ATOM	2500	CA	ALA	336	3.801	-3.441	3.845	1.00	10.26
ATOM	2501	C	ALA	336	3.301	-3.726	5.242	1.00	13.86
ATOM	2502	O	ALA	336	2.871	-4.846	5.520	1.00	12.29
ATOM	2503	CB	ALA	336	2.619	-3.179	2.912	1.00	10.63
ATOM	2504	N	VAL	337	3.422	-2.739	6.126	1.00	12.67
ATOM	2505	CA	VAL	337	2.950	-2.861	7.502	1.00	14.10

ATOM	2506	C	VAL	337	2.039	-1.664	7.756	1.00	19.06
ATOM	2507	O	VAL	337	2.387	-0.527	7.411	1.00	19.09
ATOM	2508	CB	VAL	337	4.109	-2.806	8.540	1.00	19.01
ATOM	2509	CG1	VAL	337	3.600	-3.220	9.913	1.00	18.39
ATOM	2510	CG2	VAL	337	5.263	-3.694	8.119	1.00	19.80
ATOM	2511	N	LEU	338	0.851	-1.934	8.285	1.00	13.41
ATOM	2512	CA	LEU	338	-0.119	-0.889	8.603	1.00	10.68
ATOM	2513	C	LEU	338	-0.648	-1.131	10.001	1.00	15.52
ATOM	2514	O	LEU	338	-1.226	-2.187	10.281	1.00	14.26
ATOM	2515	CB	LEU	338	-1.300	-0.901	7.624	1.00	9.01
ATOM	2516	CG	LEU	338	-2.500	-0.011	7.963	1.00	10.33
ATOM	2517	CD1	LEU	338	-2.406	1.321	7.246	1.00	8.77
ATOM	2518	CD2	LEU	338	-3.787	-0.727	7.599	1.00	12.20
ATOM	2519	N	THR	339	-0.453	-0.142	10.863	1.00	14.69
ATOM	2520	CA	THR	339	-0.914	-0.200	12.240	1.00	15.39
ATOM	2521	C	THR	339	-2.024	0.826	12.458	1.00	19.41
ATOM	2522	O	THR	339	-1.817	2.023	12.230	1.00	20.55
ATOM	2523	CB	THR	339	0.237	0.086	13.221	1.00	21.69
ATOM	2524	OG1	THR	339	1.216	-0.959	13.126	1.00	21.17
ATOM	2525	CG2	THR	339	-0.287	0.161	14.628	1.00	19.87
ATOM	2526	N	ILE	340	-3.204	0.331	12.834	1.00	14.33
ATOM	2527	CA	ILE	340	-4.389	1.141	13.123	1.00	14.67
ATOM	2528	C	ILE	340	-4.735	1.064	14.615	1.00	21.36
ATOM	2529	O	ILE	340	-4.795	-0.032	15.179	1.00	22.46
ATOM	2530	CB	ILE	340	-5.633	0.620	12.344	1.00	18.15
ATOM	2531	CG1	ILE	340	-5.412	0.751	10.839	1.00	18.38
ATOM	2532	CG2	ILE	340	-6.903	1.377	12.757	1.00	18.84
ATOM	2533	CD1	ILE	340	-5.170	2.154	10.397	1.00	20.53
ATOM	2534	N	ASP	341	-4.932	2.216	15.256	1.00	18.79
ATOM	2535	CA	ASP	341	-5.310	2.292	16.674	1.00	18.67
ATOM	2536	C	ASP	341	-6.199	3.503	16.941	1.00	19.38
ATOM	2537	O	ASP	341	-6.821	4.008	16.007	1.00	18.48
ATOM	2538	CB	ASP	341	-4.097	2.221	17.633	1.00	20.46
ATOM	2539	CG	ASP	341	-3.190	3.437	17.549	1.00	30.12
ATOM	2540	OD1	ASP	341	-3.500	4.422	16.855	1.00	34.15
ATOM	2541	OD2	ASP	341	-2.135	3.389	18.213	1.00	30.16
ATOM	2542	N	GLU	342	-6.250	3.963	18.194	1.00	14.84
ATOM	2543	CA	GLU	342	-7.093	5.095	18.591	1.00	14.95
ATOM	2544	C	GLU	342	-6.603	6.439	18.049	1.00	21.15
ATOM	2545	O	GLU	342	-7.419	7.318	17.762	1.00	19.55
ATOM	2546	CB	GLU	342	-7.283	5.157	20.111	1.00	16.06
ATOM	2547	CG	GLU	342	-8.017	3.973	20.724	1.00	20.57
ATOM	2548	CD	GLU	342	-7.121	2.773	21.007	1.00	31.58
ATOM	2549	OE1	GLU	342	-5.878	2.880	20.936	1.00	38.56
ATOM	2550	OE2	GLU	342	-7.674	1.705	21.318	1.00	1.00
ATOM	2551	N	LYS	343	-5.282	6.595	17.934	1.00	20.47
ATOM	2552	CA	LYS	343	-4.637	7.783	17.359	1.00	22.28
ATOM	2553	C	LYS	343	-3.143	7.809	17.574	1.00	35.02
ATOM	2554	O	LYS	343	-2.689	8.226	18.638	1.00	37.09
ATOM	2555	CB	LYS	343	-5.202	9.104	17.873	1.00	24.87
ATOM	2556	CG	LYS	343	-4.622	10.289	17.113	1.00	43.22
ATOM	2557	CD	LYS	343	-5.145	11.620	17.618	1.00	59.14
ATOM	2558	CE	LYS	343	-4.536	12.800	16.854	1.00	81.87
ATOM	2559	NZ	LYS	343	-5.391	14.019	16.935	1.00	93.57

ATOM	2560	N	GLY	344	-2.393	7.401	16.548	1.00 36.10
ATOM	2561	CA	GLY	344	-0.940	7.390	16.605	1.00 37.91
ATOM	2562	C	GLY	344	-0.393	7.219	18.003	1.00 47.44
ATOM	2563	O	GLY	344	-0.635	6.198	18.656	1.00 50.02
ATOM	2564	N	THR	345	0.215	8.279	18.517	1.00 44.73
ATOM	2565	CA	THR	345	0.782	8.240	19.853	1.00 45.38
ATOM	2566	C	THR	345	0.267	9.472	20.581	1.00 48.09
ATOM	2567	O	THR	345	-0.049	10.480	19.946	1.00 47.67
ATOM	2568	CB	THR	345	2.313	8.273	19.797	1.00 62.95
ATOM	2569	OG1	THR	345	2.741	9.424	19.051	1.00 67.56
ATOM	2570	CG2	THR	345	2.840	7.014	19.122	1.00 62.12
ATOM	2571	N	GLU	346	0.163	9.387	21.904	1.00 44.03
ATOM	2572	CA	GLU	346	-0.325	10.518	22.679	1.00 43.30
ATOM	2573	C	GLU	346	0.562	11.738	22.461	1.00 46.46
ATOM	2574	O	GLU	346	1.746	11.732	22.814	1.00 47.39
ATOM	2575	CB	GLU	346	-0.401	10.188	24.165	1.00 45.00
ATOM	2576	CG	GLU	346	-1.182	11.212	24.978	1.00 64.69
ATOM	2577	CD	GLU	346	-1.166	10.927	26.475	1.00108.58
ATOM	2578	OE1	GLU	346	-0.692	9.845	26.897	1.00110.00
ATOM	2579	OE2	GLU	346	-1.632	11.799	27.237	1.00110.00
ATOM	2580	N	ALA	347	-0.026	12.754	21.832	1.00 40.86
ATOM	2581	CA	ALA	347	0.634	14.021	21.536	1.00 39.63
ATOM	2582	C	ALA	347	-0.460	15.092	21.567	1.00 41.81
ATOM	2583	O	ALA	347	-1.499	14.885	22.205	1.00 42.33
ATOM	2584	CB	ALA	347	1.296	13.970	20.159	1.00 40.47
ATOM	2585	N	ALA	348	-0.235	16.231	20.879	1.00 35.47
ATOM	2586	CA	ALA	348	-1.254	17.271	20.847	1.00 34.53
ATOM	2587	C	ALA	348	-2.568	16.718	20.362	1.00 41.09
ATOM	2588	O	ALA	348	-2.750	16.513	19.173	1.00 41.40
ATOM	2589	CB	ALA	348	-0.778	18.419	19.934	1.00 34.78
ATOM	2590	N	GLY	349	-3.484	16.471	21.320	1.00 38.15
ATOM	2591	CA	GLY	349	-4.744	15.826	20.982	1.00 38.10
ATOM	2592	C	GLY	349	-5.574	16.643	20.033	1.00 41.35
ATOM	2593	O	GLY	349	-6.114	16.085	19.091	1.00 42.51
ATOM	2594	N	ALA	350	-5.673	17.965	20.291	1.00 34.71
ATOM	2595	CA	ALA	350	-6.489	18.821	19.442	1.00 33.31
ATOM	2596	C	ALA	350	-7.930	18.421	19.594	1.00 36.83
ATOM	2597	O	ALA	350	-8.424	17.591	18.846	1.00 37.89
ATOM	2598	CB	ALA	350	-6.018	18.750	17.975	1.00 33.89
ATOM	2599	N	MET	351	-8.607	19.017	20.593	1.00 30.79
ATOM	2600	CA	MET	351	-9.956	18.566	20.888	1.00 29.73
ATOM	2601	C	MET	351	-10.993	19.259	20.050	1.00 31.90
ATOM	2602	O	MET	351	-11.024	20.477	19.983	1.00 32.74
ATOM	2603	CB	MET	351	-10.280	18.653	22.394	1.00 32.16
ATOM	2604	CG	MET	351	-9.025	18.414	23.262	1.00 36.44
ATOM	2605	SD	MET	351	-8.109	16.934	22.720	1.00 41.73
ATOM	2606	CE	MET	351	-9.418	15.696	22.959	1.00 37.83
ATOM	2607	N	PHE	352	-11.848	18.447	19.401	1.00 25.13
ATOM	2608	CA	PHE	352	-12.892	19.029	18.577	1.00 23.52
ATOM	2609	C	PHE	352	-14.245	18.711	19.149	1.00 28.36
ATOM	2610	O	PHE	352	-14.342	18.020	20.150	1.00 30.86
ATOM	2611	CB	PHE	352	-12.778	18.505	17.131	1.00 25.09
ATOM	2612	CG	PHE	352	-12.827	16.979	17.095	1.00 26.88
ATOM	2613	CD1	PHE	352	-11.641	16.242	17.183	1.00 29.01

ATOM	2722	CD	LYS	365	-20.930	-4.371	16.320	1.00	16.19
ATOM	2723	CE	LYS	365	-22.013	-4.001	17.311	1.00	32.40
ATOM	2724	NZ	LYS	365	-22.746	-5.207	17.780	1.00	50.10
ATOM	2725	N	PHE	366	-17.081	-2.979	12.164	1.00	4.94
ATOM	2726	CA	PHE	366	-16.163	-3.613	11.226	1.00	5.21
ATOM	2727	C	PHE	366	-15.707	-4.870	11.942	1.00	11.04
ATOM	2728	O	PHE	366	-14.558	-4.973	12.395	1.00	9.45
ATOM	2729	CB	PHE	366	-14.990	-2.678	10.860	1.00	6.55
ATOM	2730	CG	PHE	366	-15.339	-1.691	9.761	1.00	7.39
ATOM	2731	CD1	PHE	366	-16.106	-0.565	10.039	1.00	10.00
ATOM	2732	CD2	PHE	366	-15.010	-1.954	8.436	1.00	8.12
ATOM	2733	CE1	PHE	366	-16.542	0.259	9.020	1.00	10.80
ATOM	2734	CE2	PHE	366	-15.448	-1.126	7.414	1.00	9.85
ATOM	2735	CZ	PHE	366	-16.213	-0.024	7.706	1.00	8.09
ATOM	2736	N	ASN	367	-16.675	-5.781	12.090	1.00	10.96
ATOM	2737	CA	ASN	367	-16.511	-7.057	12.775	1.00	12.66
ATOM	2738	C	ASN	367	-16.575	-8.273	11.863	1.00	20.63
ATOM	2739	O	ASN	367	-17.025	-9.343	12.274	1.00	23.39
ATOM	2740	CB	ASN	367	-17.570	-7.211	13.873	1.00	14.33
ATOM	2741	CG	ASN	367	-18.982	-7.299	13.321	1.00	53.89
ATOM	2742	OD1	ASN	367	-19.227	-7.000	12.150	1.00	45.61
ATOM	2743	ND2	ASN	367	-19.923	-7.702	14.166	1.00	57.43
ATOM	2744	N	LYS	368	-16.183	-8.100	10.612	1.00	15.70
ATOM	2745	CA	LYS	368	-16.163	-9.201	9.648	1.00	15.30
ATOM	2746	C	LYS	368	-15.231	-8.792	8.508	1.00	23.90
ATOM	2747	O	LYS	368	-14.900	-7.595	8.372	1.00	25.23
ATOM	2748	CB	LYS	368	-17.577	-9.530	9.149	1.00	14.67
ATOM	2749	CG	LYS	368	-18.279	-8.405	8.423	1.00	5.03
ATOM	2750	CD	LYS	368	-19.624	-8.855	7.894	1.00	2.48
ATOM	2751	CE	LYS	368	-20.409	-7.697	7.293	1.00	26.14
ATOM	2752	NZ	LYS	368	-21.767	-8.081	6.805	1.00	49.97
ATOM	2753	N	PRO	369	-14.826	-9.751	7.652	1.00	18.79
ATOM	2754	CA	PRO	369	-13.927	-9.382	6.567	1.00	17.06
ATOM	2755	C	PRO	369	-14.315	-8.087	5.846	1.00	15.58
ATOM	2756	O	PRO	369	-15.498	-7.832	5.590	1.00	13.98
ATOM	2757	CB	PRO	369	-13.959	-10.625	5.682	1.00	18.58
ATOM	2758	CG	PRO	369	-14.067	-11.718	6.699	1.00	22.28
ATOM	2759	CD	PRO	369	-15.202	-11.174	7.525	1.00	17.81
ATOM	2760	N	PHE	370	-13.335	-7.198	5.698	1.00	10.74
ATOM	2761	CA	PHE	370	-13.554	-5.924	4.999	1.00	9.37
ATOM	2762	C	PHE	370	-12.338	-5.508	4.178	1.00	7.98
ATOM	2763	O	PHE	370	-11.206	-5.867	4.520	1.00	6.62
ATOM	2764	CB	PHE	370	-13.946	-4.795	5.979	1.00	10.78
ATOM	2765	CG	PHE	370	-12.879	-4.437	6.990	1.00	10.60
ATOM	2766	CD1	PHE	370	-11.902	-3.492	6.695	1.00	12.76
ATOM	2767	CD2	PHE	370	-12.861	-5.047	8.236	1.00	11.98
ATOM	2768	CE1	PHE	370	-10.918	-3.157	7.629	1.00	13.14
ATOM	2769	CE2	PHE	370	-11.888	-4.725	9.176	1.00	15.00
ATOM	2770	CZ	PHE	370	-10.910	-3.779	8.872	1.00	13.05
ATOM	2771	N	VAL	371	-12.564	-4.811	3.067	1.00	3.46
ATOM	2772	CA	VAL	371	-11.444	-4.329	2.256	1.00	4.17
ATOM	2773	C	VAL	371	-11.239	-2.845	2.601	1.00	6.84
ATOM	2774	O	VAL	371	-12.083	-2.249	3.258	1.00	6.12
ATOM	2775	CB	VAL	371	-11.695	-4.504	0.720	1.00	9.05

ATOM	2776	CG1	VAL	371	-12.221	-5.900	0.425	1.00	9.32
ATOM	2777	CG2	VAL	371	-12.624	-3.438	0.175	1.00	8.76
ATOM	2778	N	PHE	372	-10.132	-2.250	2.181	1.00	6.72
ATOM	2779	CA	PHE	372	-9.886	-0.839	2.476	1.00	8.81
ATOM	2780	C	PHE	372	-8.708	-0.283	1.693	1.00	10.01
ATOM	2781	O	PHE	372	-7.897	-1.043	1.163	1.00	10.68
ATOM	2782	CB	PHE	372	-9.618	-0.649	3.966	1.00	12.58
ATOM	2783	CG	PHE	372	-8.354	-1.286	4.422	1.00	15.84
ATOM	2784	CD1	PHE	372	-8.308	-2.658	4.636	1.00	21.46
ATOM	2785	CD2	PHE	372	-7.189	-0.543	4.547	1.00	18.60
ATOM	2786	CE1	PHE	372	-7.122	-3.283	4.960	1.00	22.91
ATOM	2787	CE2	PHE	372	-5.997	-1.158	4.869	1.00	22.97
ATOM	2788	CZ	PHE	372	-5.966	-2.534	5.075	1.00	22.13
ATOM	2789	N	LEU	373	-8.612	1.040	1.616	1.00	4.88
ATOM	2790	CA	LEU	373	-7.509	1.687	0.895	1.00	4.91
ATOM	2791	C	LEU	373	-7.125	2.944	1.636	1.00	9.95
ATOM	2792	O	LEU	373	-7.918	3.481	2.393	1.00	9.65
ATOM	2793	CB	LEU	373	-7.912	2.092	-0.532	1.00	4.96
ATOM	2794	CG	LEU	373	-8.335	1.061	-1.579	1.00	10.99
ATOM	2795	CD1	LEU	373	-9.789	0.654	-1.396	1.00	11.13
ATOM	2796	CD2	LEU	373	-8.135	1.658	-2.946	1.00	17.94
ATOM	2797	N	MET	374	-5.882	3.368	1.467	1.00	9.56
ATOM	2798	CA	MET	374	-5.394	4.597	2.083	1.00	11.81
ATOM	2799	C	MET	374	-4.968	5.441	0.890	1.00	14.51
ATOM	2800	O	MET	374	-4.134	5.011	0.082	1.00	12.10
ATOM	2801	CB	MET	374	-4.215	4.349	3.040	1.00	15.63
ATOM	2802	CG	MET	374	-4.611	3.932	4.459	1.00	20.55
ATOM	2803	SD	MET	374	-5.417	2.313	4.607	1.00	26.18
ATOM	2804	CE	MET	374	-6.308	2.489	6.158	1.00	22.81
ATOM	2805	N	ILE	375	-5.608	6.600	0.749	1.00	11.32
ATOM	2806	CA	ILE	375	-5.376	7.518	-0.355	1.00	10.65
ATOM	2807	C	ILE	375	-4.724	8.807	0.112	1.00	15.85
ATOM	2808	O	ILE	375	-5.187	9.404	1.076	1.00	15.31
ATOM	2809	CB	ILE	375	-6.727	7.883	-1.039	1.00	13.28
ATOM	2810	CG1	ILE	375	-7.222	6.742	-1.928	1.00	13.42
ATOM	2811	CG2	ILE	375	-6.589	9.148	-1.867	1.00	15.20
ATOM	2812	CD1	ILE	375	-7.874	5.633	-1.180	1.00	22.33
ATOM	2813	N	GLU	376	-3.656	9.238	-0.563	1.00	14.38
ATOM	2814	CA	GLU	376	-3.002	10.503	-0.212	1.00	14.97
ATOM	2815	C	GLU	376	-3.920	11.596	-0.767	1.00	19.93
ATOM	2816	O	GLU	376	-4.048	11.755	-1.976	1.00	17.98
ATOM	2817	CB	GLU	376	-1.603	10.607	-0.842	1.00	16.23
ATOM	2818	CG	GLU	376	-0.710	11.742	-0.291	1.00	21.49
ATOM	2819	CD	GLU	376	-1.097	13.127	-0.798	1.00	33.08
ATOM	2820	OE1	GLU	376	-1.086	13.331	-2.033	1.00	18.50
ATOM	2821	OE2	GLU	376	-1.377	14.023	0.021	1.00	13.34
ATOM	2822	N	GLN	377	-4.550	12.337	0.136	1.00	19.62
ATOM	2823	CA	GLN	377	-5.492	13.396	-0.202	1.00	20.97
ATOM	2824	C	GLN	377	-5.247	14.235	-1.451	1.00	27.18
ATOM	2825	O	GLN	377	-6.191	14.510	-2.197	1.00	27.14
ATOM	2826	CB	GLN	377	-5.676	14.337	0.985	1.00	22.95
ATOM	2827	CG	GLN	377	-6.428	13.737	2.162	1.00	53.08
ATOM	2828	CD	GLN	377	-6.529	14.707	3.319	1.00	88.55
ATOM	2829	OE1	GLN	377	-6.140	15.874	3.205	1.00	89.13

ATOM	2830	NE2	GLN	377	-7.044	14.235	4.442	1.00	87.27
ATOM	2831	N	ASN	378	-3.994	14.628	-1.686	1.00	25.79
ATOM	2832	CA	ASN	378	-3.653	15.485	-2.837	1.00	26.20
ATOM	2833	C	ASN	378	-3.532	14.842	-4.220	1.00	24.55
ATOM	2834	O	ASN	378	-4.119	15.319	-5.203	1.00	22.77
ATOM	2835	CB	ASN	378	-2.371	16.277	-2.553	1.00	31.43
ATOM	2836	CG	ASN	378	-2.525	17.214	-1.398	1.00	65.73
ATOM	2837	OD1	ASN	378	-3.258	18.197	-1.478	1.00	65.38
ATOM	2838	ND2	ASN	378	-1.840	16.920	-0.305	1.00	59.75
ATOM	2839	N	THR	379	-2.750	13.773	-4.281	1.00	16.72
ATOM	2840	CA	THR	379	-2.496	13.058	-5.520	1.00	14.54
ATOM	2841	C	THR	379	-3.531	11.954	-5.732	1.00	16.01
ATOM	2842	O	THR	379	-3.682	11.435	-6.830	1.00	14.59
ATOM	2843	CB	THR	379	-1.141	12.415	-5.428	1.00	27.00
ATOM	2844	OG1	THR	379	-1.168	11.474	-4.345	1.00	35.99
ATOM	2845	CG2	THR	379	-0.078	13.478	-5.109	1.00	27.54
ATOM	2846	N	LYS	380	-4.190	11.559	-4.650	1.00	12.96
ATOM	2847	CA	LYS	380	-5.186	10.495	-4.669	1.00	11.20
ATOM	2848	C	LYS	380	-4.569	9.158	-5.066	1.00	14.14
ATOM	2849	O	LYS	380	-5.264	8.247	-5.507	1.00	14.84
ATOM	2850	CB	LYS	380	-6.359	10.874	-5.554	1.00	13.33
ATOM	2851	CG	LYS	380	-7.021	12.147	-5.076	1.00	43.92
ATOM	2852	CD	LYS	380	-8.294	12.466	-5.834	1.00	62.33
ATOM	2853	CE	LYS	380	-8.943	13.746	-5.320	1.00	75.41
ATOM	2854	NZ	LYS	380	-10.179	14.084	-6.069	1.00	81.22
ATOM	2855	N	SER	381	-3.267	9.033	-4.806	1.00	10.76
ATOM	2856	CA	SER	381	-2.501	7.829	-5.078	1.00	10.64
ATOM	2857	C	SER	381	-2.826	6.773	-4.043	1.00	17.98
ATOM	2858	O	SER	381	-2.763	7.035	-2.825	1.00	18.86
ATOM	2859	CB	SER	381	-1.009	8.137	-5.013	1.00	12.65
ATOM	2860	OG	SER	381	-0.681	9.193	-5.890	1.00	24.22
ATOM	2861	N	PRO	382	-3.165	5.556	-4.498	1.00	15.96
ATOM	2862	CA	PRO	382	-3.484	4.522	-3.516	1.00	15.23
ATOM	2863	C	PRO	382	-2.229	4.026	-2.787	1.00	15.86
ATOM	2864	O	PRO	382	-1.428	3.275	-3.343	1.00	13.97
ATOM	2865	CB	PRO	382	-4.191	3.461	-4.359	1.00	16.74
ATOM	2866	CG	PRO	382	-3.507	3.573	-5.698	1.00	21.91
ATOM	2867	CD	PRO	382	-3.367	5.069	-5.880	1.00	17.13
ATOM	2868	N	LEU	383	-2.046	4.542	-1.572	1.00	11.15
ATOM	2869	CA	LEU	383	-0.918	4.229	-0.704	1.00	10.25
ATOM	2870	C	LEU	383	-0.941	2.803	-0.201	1.00	15.69
ATOM	2871	O	LEU	383	0.078	2.122	-0.202	1.00	17.23
ATOM	2872	CB	LEU	383	-0.886	5.190	0.494	1.00	9.55
ATOM	2873	CG	LEU	383	-0.330	6.617	0.332	1.00	12.09
ATOM	2874	CD1	LEU	383	-0.693	7.455	1.530	1.00	11.38
ATOM	2875	CD2	LEU	383	1.174	6.596	0.129	1.00	12.37
ATOM	2876	N	PHE	384	-2.105	2.345	0.221	1.00	9.64
ATOM	2877	CA	PHE	384	-2.237	0.991	0.733	1.00	7.84
ATOM	2878	C	PHE	384	-3.581	0.451	0.283	1.00	13.29
ATOM	2879	O	PHE	384	-4.559	1.202	0.192	1.00	14.82
ATOM	2880	CB	PHE	384	-2.279	0.989	2.272	1.00	8.59
ATOM	2881	CG	PHE	384	-0.933	1.120	2.952	1.00	9.77
ATOM	2882	CD1	PHE	384	-0.204	-0.013	3.291	1.00	12.34
ATOM	2883	CD2	PHE	384	-0.418	2.367	3.311	1.00	11.86

ATOM	2884	CE1	PHE	384	1.004	0.085	3.979	1.00	12.93
ATOM	2885	CE2	PHE	384	0.789	2.468	3.997	1.00	14.08
ATOM	2886	CZ	PHE	384	1.501	1.327	4.330	1.00	12.25
ATOM	2887	N	MET	385	-3.618	-0.834	-0.042	1.00	7.74
ATOM	2888	CA	MET	385	-4.868	-1.496	-0.373	1.00	6.20
ATOM	2889	C	MET	385	-4.769	-2.816	0.368	1.00	5.90
ATOM	2890	O	MET	385	-3.680	-3.368	0.518	1.00	2.53
ATOM	2891	CB	MET	385	-5.069	-1.722	-1.877	1.00	8.34
ATOM	2892	CG	MET	385	-6.406	-2.403	-2.150	1.00	11.63
ATOM	2893	SD	MET	385	-7.016	-2.177	-3.806	1.00	15.95
ATOM	2894	CE	MET	385	-8.683	-2.637	-3.625	1.00	12.69
ATOM	2895	N	GLY	386	-5.890	-3.290	0.887	1.00	2.67
ATOM	2896	CA	GLY	386	-5.870	-4.544	1.597	1.00	2.61
ATOM	2897	C	GLY	386	-7.235	-5.010	2.027	1.00	8.66
ATOM	2898	O	GLY	386	-8.228	-4.350	1.761	1.00	8.72
ATOM	2899	N	LYS	387	-7.274	-6.176	2.658	1.00	9.06
ATOM	2900	CA	LYS	387	-8.501	-6.778	3.168	1.00	9.44
ATOM	2901	C	LYS	387	-8.129	-7.460	4.468	1.00	14.80
ATOM	2902	O	LYS	387	-7.091	-8.115	4.559	1.00	14.15
ATOM	2903	CB	LYS	387	-9.067	-7.823	2.195	1.00	10.21
ATOM	2904	CG	LYS	387	-10.168	-8.686	2.800	1.00	10.53
ATOM	2905	CD	LYS	387	-10.771	-9.628	1.789	1.00	17.82
ATOM	2906	CE	LYS	387	-9.741	-10.614	1.280	1.00	30.69
ATOM	2907	NZ	LYS	387	-10.341	-11.615	0.359	1.00	46.30
ATOM	2908	N	VAL	388	-8.937	-7.231	5.493	1.00	12.28
ATOM	2909	CA	VAL	388	-8.718	-7.849	6.782	1.00	11.26
ATOM	2910	C	VAL	388	-9.748	-8.959	6.904	1.00	14.50
ATOM	2911	O	VAL	388	-10.952	-8.720	6.825	1.00	12.32
ATOM	2912	CB	VAL	388	-8.852	-6.834	7.952	1.00	14.78
ATOM	2913	CG1	VAL	388	-8.686	-7.539	9.285	1.00	14.30
ATOM	2914	CG2	VAL	388	-7.802	-5.738	7.818	1.00	14.55
ATOM	2915	N	VAL	389	-9.251	-10.186	6.900	1.00	14.18
ATOM	2916	CA	VAL	389	-10.092	-11.356	7.043	1.00	15.05
ATOM	2917	C	VAL	389	-10.113	-11.638	8.545	1.00	23.37
ATOM	2918	O	VAL	389	-11.181	-11.822	9.135	1.00	25.50
ATOM	2919	CB	VAL	389	-9.535	-12.590	6.237	1.00	18.20
ATOM	2920	CG1	VAL	389	-9.645	-12.354	4.747	1.00	17.82
ATOM	2921	CG2	VAL	389	-8.089	-12.863	6.580	1.00	18.27
ATOM	2922	N	ASN	390	-8.945	-11.515	9.182	1.00	20.60
ATOM	2923	CA	ASN	390	-8.809	-11.769	10.622	1.00	20.91
ATOM	2924	C	ASN	390	-7.641	-10.999	11.240	1.00	23.96
ATOM	2925	O	ASN	390	-6.472	-11.335	11.010	1.00	23.22
ATOM	2926	CB	ASN	390	-8.623	-13.266	10.865	1.00	26.08
ATOM	2927	CG	ASN	390	-8.801	-13.652	12.312	1.00	56.92
ATOM	2928	OD1	ASN	390	-8.664	-12.831	13.221	1.00	66.14
ATOM	2929	ND2	ASN	390	-9.114	-14.917	12.540	1.00	41.21
ATOM	2930	N	PRO	391	-7.946	-10.034	12.127	1.00	20.72
ATOM	2931	CA	PRO	391	-6.941	-9.213	12.789	1.00	20.87
ATOM	2932	C	PRO	391	-5.886	-10.027	13.503	1.00	31.97
ATOM	2933	O	PRO	391	-4.750	-9.585	13.641	1.00	33.17
ATOM	2934	CB	PRO	391	-7.776	-8.394	13.765	1.00	21.61
ATOM	2935	CG	PRO	391	-9.039	-8.187	12.996	1.00	25.72
ATOM	2936	CD	PRO	391	-9.286	-9.624	12.588	1.00	21.28
ATOM	2937	N	THR	392	-6.269	-11.230	13.910	1.00	33.77

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ATOM   2938  CA  THR   392      -5.388 -12.134  14.630  1.00 35.56
ATOM   2939  C   THR   392      -4.138 -12.469  13.823  1.00 41.19
ATOM   2940  O   THR   392      -3.042 -12.602  14.379  1.00 42.51
ATOM   2941  CB  THR   392      -6.136 -13.423  15.015  1.00 56.77
ATOM   2942  OG1 THR   392      -7.263 -13.091  15.843  1.00 59.19
ATOM   2943  CG2 THR   392      -5.219 -14.371  15.764  1.00 61.71
ATOM   2944  N   GLN   393      -4.299 -12.591  12.512  1.00 36.59
ATOM   2945  CA  GLN   393      -3.174 -12.891  11.639  1.00 36.28
ATOM   2946  C   GLN   393      -2.345 -11.630  11.429  1.00 43.21
ATOM   2947  O   GLN   393      -2.894 -10.531  11.321  1.00 44.40
ATOM   2948  CB  GLN   393      -3.684 -13.393  10.290  1.00 37.18
ATOM   2949  CG  GLN   393      -2.609 -13.457   9.206  1.00 38.11
ATOM   2950  CD  GLN   393      -3.165 -13.823   7.853  1.00 59.92
ATOM   2951  OE1 GLN   393      -4.385 -13.831   7.634  1.00 50.05
ATOM   2952  NE2 GLN   393      -2.275 -14.108   6.921  1.00 61.15
ATOM   2953  N   LYS   394      -1.029 -11.792  11.357  1.00 41.17
ATOM   2954  CA  LYS   394      -0.136 -10.663  11.122  1.00 73.90
ATOM   2955  C   LYS   394       1.066 -11.069  10.275  1.00106.52
ATOM   2956  O   LYS   394       1.137 -12.250   9.864  1.00 66.01
ATOM   2957  CB  LYS   394       0.337 -10.042  12.437  1.00 76.30
ATOM   2958  CG  LYS   394       1.231  -8.828  12.249  1.00 89.36
ATOM   2959  CD  LYS   394       1.763  -8.284  13.564  1.00 97.21
ATOM   2960  CE  LYS   394       2.652  -7.066  13.337  1.00100.59
ATOM   2961  NZ  LYS   394       3.234  -6.531  14.594  1.00101.87
ATOM   2962  OXT LYS   394       1.924 -10.199   9.997  1.00 66.01
TER    2963      LYS   394
HETATM 2964  S   SCC     1     -22.279   4.447  -3.715  1.00 31.26
HETATM 2965  C1  SCC     1     -23.852   4.645  -4.634  1.00 27.60
HETATM 2966  C2  SCC     1     -23.920   5.944  -5.448  1.00 26.84
CONECT 1693 1692 2964
CONECT 2964 1693 2965
CONECT 2965 2964 2966
CONECT 2966 2965
MASTER        0    0    0    0    0    0    0    0 2965    1    4   29
END
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We claim:

1. A furin endoprotease inhibitor comprising a mimetic compound to that portion of α_1-antitrypsin Portland that comprises amino acid sequence Arg-Xaa-Xaa-Arg at positions 355 through 358 of the amino acid sequence of α_1-antitrypsin Portland, wherein the atoms of said mimetic are arranged in three dimensional conformation at positions equivalent to those of the atoms comprising the amino acid sequence Arg-Xaa-Xaa-Arg.

2. A homogenous composition of matter comprising a mimetic compound to that portion of α_1-antitrypsin Portland that comprises an amino acid sequence Arg-Xaa-Xaa-Arg at positions 355 through 358 of the amino acid sequence of α_1-antitrypsin Portland, wherein the atoms of said mimetic are arranged in three dimensional conformation at positions equivalent to those of the atoms comprising the amino acid sequence Arg-Xaa-Xaa-Arg.

3. A method of blocking endoproteolytic activation of a bacterial toxin comprising the step of contacting a cell in the presence of the toxin with a furin endoprotease inhibitor according to Claim 1.

4. The method of Claim 3 wherein the bacterial toxin is diphtheria toxin of *Corynebacterium diptheriae*.

5. The method of Claim 3 wherein the bacterial toxin is anthrax toxin of *Bacillus anthracis*.

6. The method of Claim 3 wherein the bacterial toxin is *Pseudomonas aeruginosa* exotoxin.

7. A pharmaceutical composition comprising a therapeutically effective amount of a furin endoprotease inhibitor of Claim 1 and a pharmaceutically acceptable carrier or diluent.

8. A method of inhibiting bacterial infection of cells comprising contacting the cells with a furin endoprotease inhibitor according to Claim 1.

9. The method of Claim 8 wherein the bacterial toxin is diphtheria toxin of *Corynebacterium diptheriae*.

10. The method of Claim 8 wherein the bacterial toxin is anthrax toxin of *Bacillus anthracis*.

11. The method of Claim 8 wherein the bacterial toxin is *Pseudomonas aeruginosa* exotoxin.

12. A method of inhibiting viral infection of cells comprising contacting the cells with a furin endoprotease inhibitor according to Claim 1.

13. The method of Claim 12 wherein the virus is cytomegalovirus.

14. A method of blocking endoproteolytic viral protein maturation comprising the step of contacting a cell in the presence of the toxin with a furin endoprotease inhibitor according to Claim 1.

15. The method of Claim 14 wherein the virus is cytomegalovirus.

16. A pharmaceutical composition according to Claim 7, further comprising an antibacterial compound.

17. A pharmaceutical composition according to Claim 7, further comprising an antiviral compound.

18. A furin endoprotease inhibitor comprising a mimetic compound having the structure:

C(L1-R1)-E-F-G-H-I-J(L2-R2)

wherein " "C" is a mimetic element that is equivalent to a first alpha carbon;

"J" is a mimetic element that is equivalent to a second alpha carbon;

whereby "C" and "J" are conformationally hindered;

"E", "G", and "I" are planar moieties having dimensions substantially similar to a peptide bond;

"F" and "H" are mimetic elements that are each equivalent to a conformationally-hindered alpha carbons;

wherein either "F" or "H" are restricted by being integrally covalently linked to a cyclic planar moiety selected from the group consisting of cyclopentane, cyclopentene, furan, tetrahydrofuran, thiophene, pyrrole, or pyrrolidine, or wherein "F" or "H" is covalently linked to a sterically-hindered group;

and whereby E-F-G-H-I is most preferably substantially planar and deviates from this planar structure by no more than from about 1 to about 20 degrees from said plane and wherein the length of the molecule along the distance between the "C" and "J" components (C-E-F-G-H-I-J) is preferably from about 7.5 to about 11.5 Angstroms;

R1 and R2 are each positively-charged residues;

L1 and L2 are each linker moieties selected from the group consisting of methylenes and mimetic elements equivalent thereto;

wherein R1 and R2 are from about 5 to about 7 Angstroms away from their respective alpha carbon equivalents, "C" and "J";

and whereby R1 and R2 are displaced relative to each other along the longitudinal axis of the molecule to subtend an angle of from about 15 to about 25 degrees.

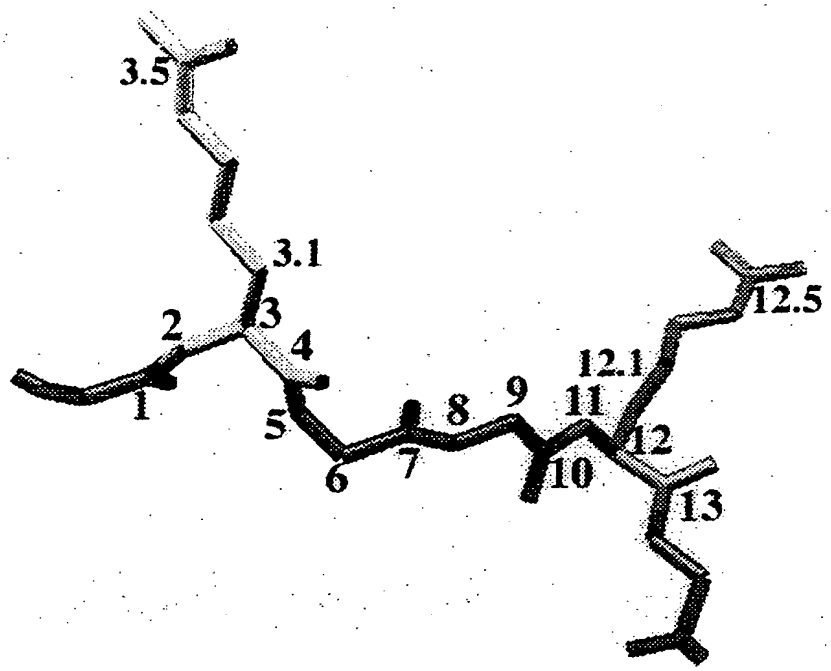

Figure 1A

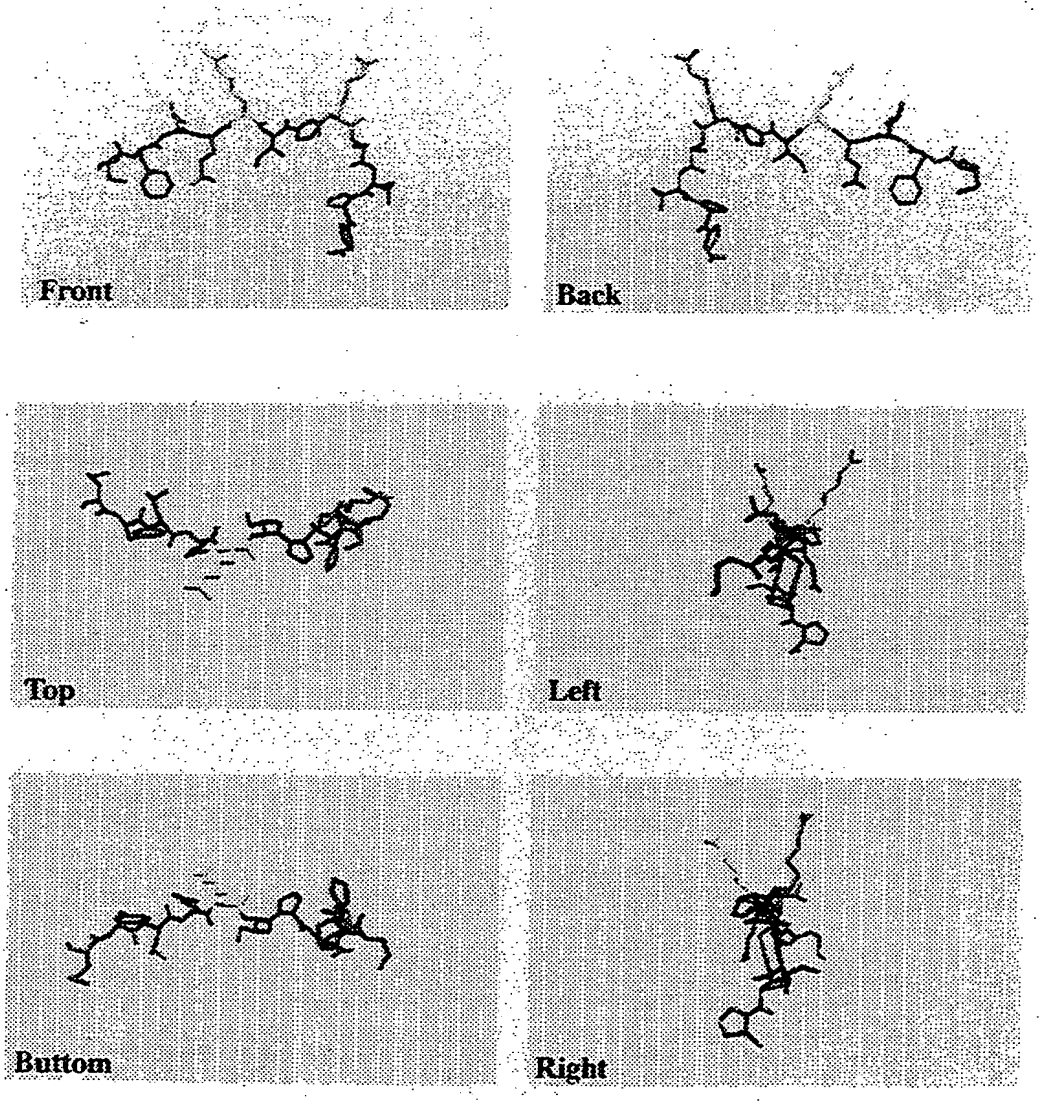

Figure 1B

ROPPe279
Ia
II+Ib
III
613
Pseudomonas exotoxin A
Protoxin from Pseudomonas aeruginosa
Cleaved by furin in endosomes
Pseudomonas aeruginosa
Major complication in:
Burn patients
Cystic fibrosis patients
RTKR465
TM
906
Pro
HCMV glycoprotein gB
Virion-associated protein
Cleaved by furin
Human Cytomegalovirus
Major cause of morbidity and mortality in immunocompromised individuals transplant and AIDS patients
ER
Golgi
TGN
HCMV gB
PEA
Endocytic Pathway
Constitutive Pathway

FIGURE 2

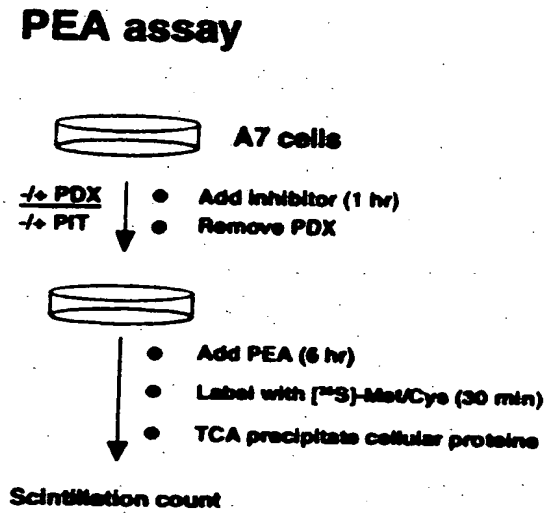
PEA assay
A7 cells
-/+ PDX
-/+ PIT
Add inhibitor (1 hr)
Remove PDX
Add PEA (6 hr)
Label with [35S]-Met/Cys (30 min)
TCA precipitate cellular proteins
Scintillation count

FIGURE 3

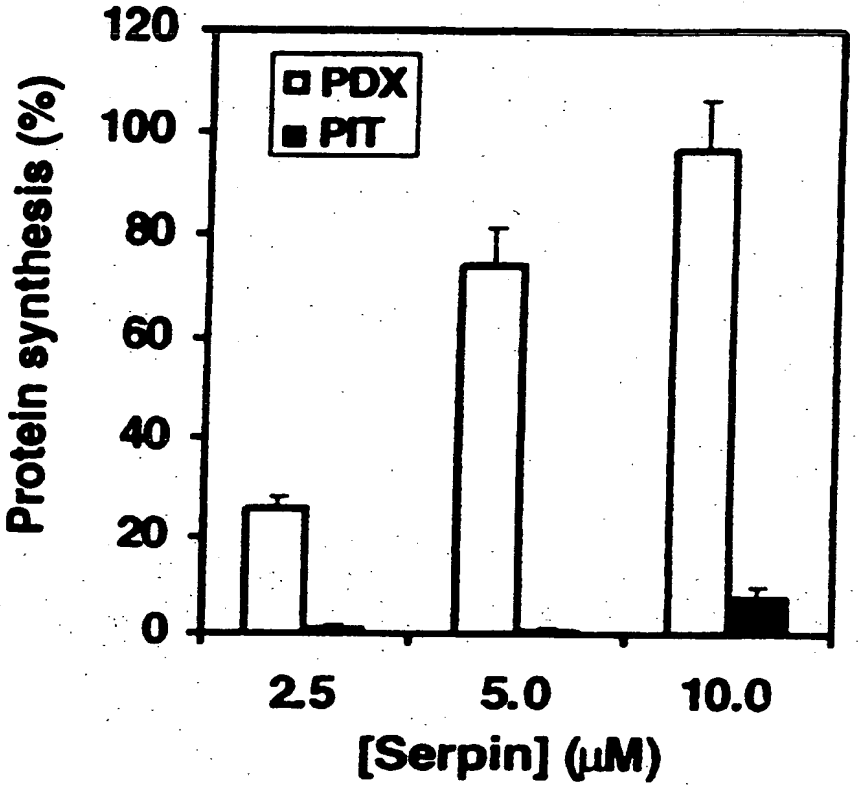
120
100
80
60
40
20
0
Protein synthesis (%)
PDX
PIT
2.5
5.0
10.0
[Serpin] (μM)

FIGURE 4

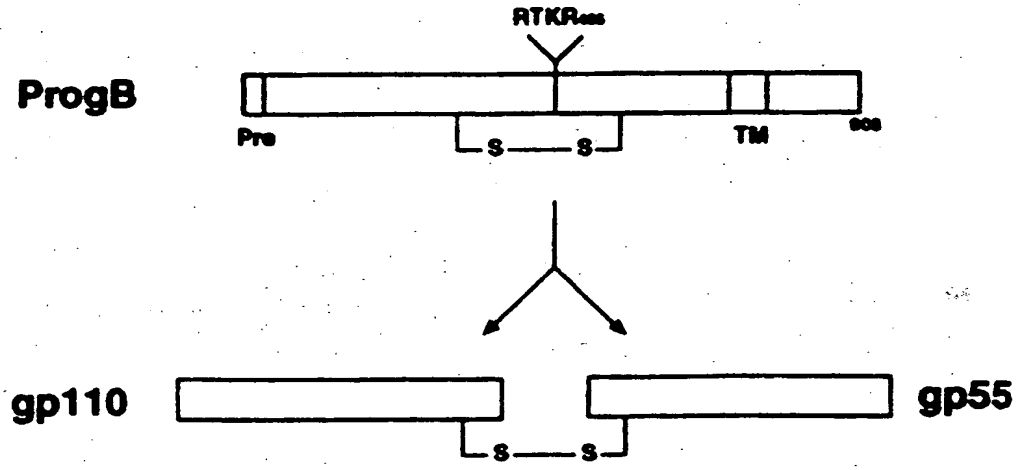

FIGURE 5

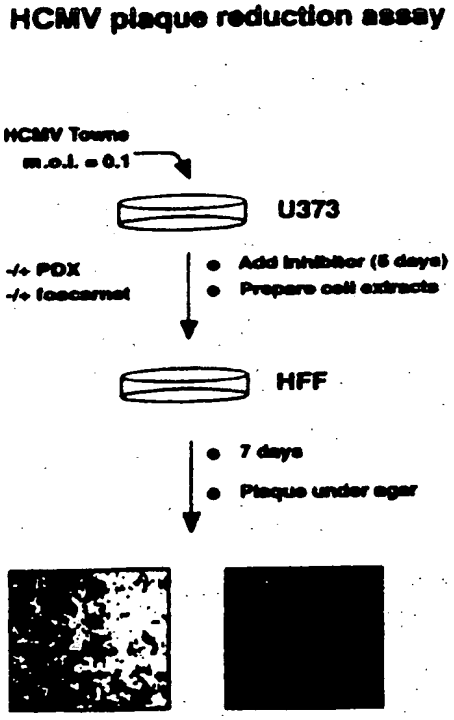
HCMV plaque reduction assay
HCMV Towne
m.o.i. = 0.1
U373
-/+ PDX
-/+ foscarnet
Add inhibitor (6 days)
Prepare cell extracts
HFF
7 days
Plaque under agar

FIGURE 6

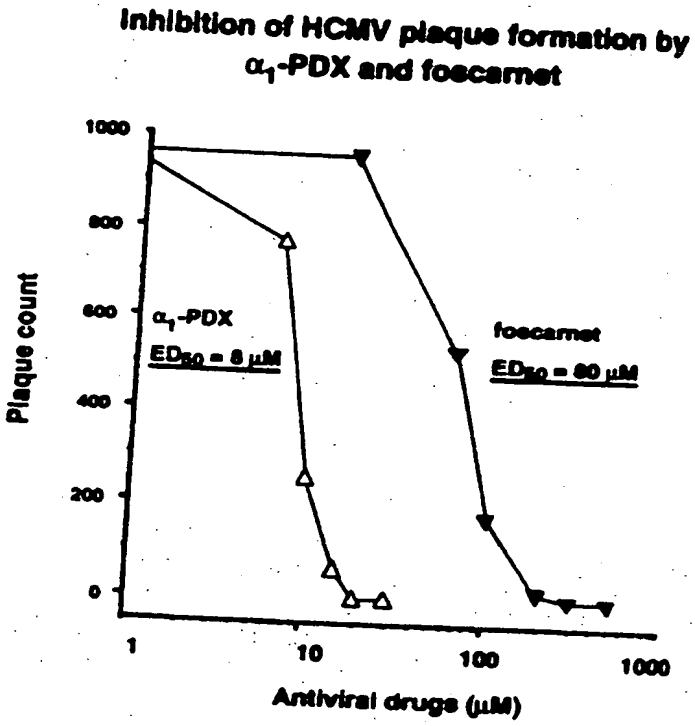
Inhibition of HCMV plaque formation by
α_1-PDX and foscarnet
Plaque count
1000
800
600
400
200
0
α_1-PDX
ED_{50} = 8 µM
foscarnet
ED_{50} = 80 µM
1
10
100
1000
Antiviral drugs (µM)

FIGURE 7

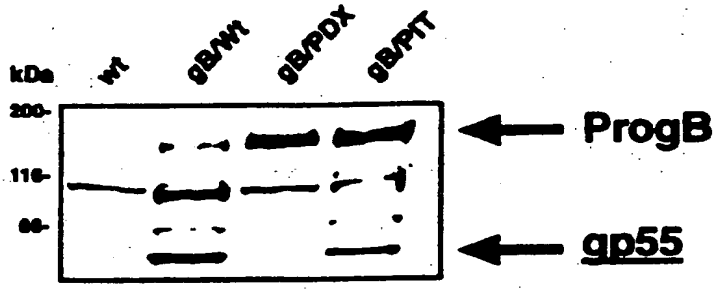

FIGURE 8

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Jean, Francois
Thomas, Gary

(ii) TITLE OF INVENTION: Methods and Reagents for Inhibiting Furin Endoprotease

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
(B) STREET: 300 South Wacker Drive
(C) CITY: Chicago
(D) STATE: IL
(E) COUNTRY: USA
(F) ZIP: 60606

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US
(B) FILING DATE: 08-APR-1999
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Noonan, Kevin E
(B) REGISTRATION NUMBER: 35,303
(C) REFERENCE/DOCKET NUMBER: 92,448-H

(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 312-913-0001
(B) TELEFAX: 312-913-0002
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Modified site
(B) LOCATION: 355..358
(C) OTHER INFORMATION: /label=Variant
/ note="The amino acid sequence is the amino acid sequence of the modified alpha-1-antitrypsin protein, alpha-1-antitrypsin Portland."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser His His
1 5 10 15

Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu
20 25 30

Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr
35 40 45

```
Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu
 50                  55                  60

Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu Gly Leu
65                  70                  75                  80

Asn Phe Asn Leu Thr Gln Ile Pro Glu Ala Gln Ile His Glu Gly Phe
                85                  90                  95

Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu Gln Leu
            100                 105                 110

Thr Thr Gly Asn Gly Leu Phe Leu Ser Gln Gly Leu Lys Leu Val Asp
        115                 120                 125

Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr
    130                 135                 140

Val Asn Phe Gly Asp Thr Glu Gln Ala Lys Lys Gln Ile Asn Asp Tyr
145                 150                 155                 160

Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu
                165                 170                 175

Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe Lys Gly
            180                 185                 190

Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu Asp Phe
        195                 200                 205

His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys Arg Leu
    210                 215                 220

Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp Val Leu
225                 230                 235                 240

Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro Asp
                245                 250                 255

Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile
            260                 265                 270

Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu His Leu
        275                 280                 285

Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly
    290                 295                 300

Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly Ala Asp Leu Ser Gly
305                 310                 315                 320

Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys Ala Val His Lys Ala
                325                 330                 335

Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala Met Phe
            340                 345                 350

Leu Glu Arg Ile Pro Arg Ser Ile Pro Pro Glu Val Lys Phe Asn Lys
        355                 360                 365

Pro Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe
    370                 375                 380

Met Gly Lys Val Val Asn Pro Thr Gly Lys
385                 390
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Ile Pro Met
1

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Arg Ile Pro Arg
1

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified site
(B) LOCATION: 2..3
(C) OTHER INFORMATION: /label=Variable site
/ note="The amino acid Xaa at position 2 can be any amino acid; the amino acid Xaa at position 3 can be any amino acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Xaa Xaa Arg
1

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(A) NAME/KEY: Modified site
(B) LOCATION: 2..3
(C) OTHER INFORMATION: /label=Variable site
/ note="The amino acid Xaa at position 2 can be any amino acid."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Arg Xaa Pro Arg
1

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 394 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Modified site
(B) LOCATION: 355..358
(C) OTHER INFORMATION: /label=Variant
/ note="The amino acid sequence is the amino acid sequence of the modified alpha-1-antitrypsin protein, alpha-1-antitrypsin Pittsburgh."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Asp Pro Gln Gly Asp Ala Ala Gln Lys Thr Asp Thr Ser His His
1 5 10 15

Asp Gln Asp His Pro Thr Phe Asn Lys Ile Thr Pro Asn Leu Ala Glu
20 25 30

Phe Ala Phe Ser Leu Tyr Arg Gln Leu Ala His Gln Ser Asn Ser Thr
35 40 45

Asn Ile Phe Phe Ser Pro Val Ser Ile Ala Thr Ala Phe Ala Met Leu
50 55 60

Ser Leu Gly Thr Lys Ala Asp Thr His Asp Glu Ile Leu Glu Gly Leu
65 70 75 80

Asn Phe Asn Leu Thr Gln Ile Pro Glu Ala Gln Ile His Glu Gly Phe
85 90 95

Gln Glu Leu Leu Arg Thr Leu Asn Gln Pro Asp Ser Gln Leu Gln Leu
100 105 110

Thr Thr Gly Asn Gly Leu Phe Leu Ser Gln Gly Leu Lys Leu Val Asp
115 120 125

Lys Phe Leu Glu Asp Val Lys Lys Leu Tyr His Ser Glu Ala Phe Thr
130 135 140

Val Asn Phe Gly Asp Thr Glu Gln Ala Lys Lys Gln Ile Asn Asp Tyr
145 150 155 160

Val Glu Lys Gly Thr Gln Gly Lys Ile Val Asp Leu Val Lys Glu Leu
165 170 175

Asp Arg Asp Thr Val Phe Ala Leu Val Asn Tyr Ile Phe Phe Lys Gly
180 185 190

```
Lys Trp Glu Arg Pro Phe Glu Val Lys Asp Thr Glu Glu Glu Asp Phe
        195                 200                 205

His Val Asp Gln Val Thr Thr Val Lys Val Pro Met Met Lys Arg Leu
    210                 215                 220

Gly Met Phe Asn Ile Gln His Cys Lys Lys Leu Ser Ser Trp Val Leu
225                 230                 235                 240

Leu Met Lys Tyr Leu Gly Asn Ala Thr Ala Ile Phe Phe Leu Pro Asp
                245                 250                 255

Glu Gly Lys Leu Gln His Leu Glu Asn Glu Leu Thr His Asp Ile Ile
            260                 265                 270

Thr Lys Phe Leu Glu Asn Glu Asp Arg Arg Ser Ala Ser Leu His Leu
        275                 280                 285

Pro Lys Leu Ser Ile Thr Gly Thr Tyr Asp Leu Lys Ser Val Leu Gly
    290                 295                 300

Gln Leu Gly Ile Thr Lys Val Phe Ser Asn Gly Ala Asp Leu Ser Gly
305                 310                 315                 320

Val Thr Glu Glu Ala Pro Leu Lys Leu Ser Lys Ala Val His Lys Ala
                325                 330                 335

Val Leu Thr Ile Asp Glu Lys Gly Thr Glu Ala Ala Gly Ala Met Phe
            340                 345                 350

Leu Glu Ala Ile Pro Arg Ser Ile Pro Pro Glu Val Lys Phe Asn Lys
        355                 360                 365

Pro Phe Val Phe Leu Met Ile Glu Gln Asn Thr Lys Ser Pro Leu Phe
    370                 375                 380

Met Gly Lys Val Val Asn Pro Thr Gly Lys
385                 390
```